

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 29, 2002, 15:43:21 ; Search time 20.72 Seconds  
(without alignments)  
195.688 Million cell updates/sec

Title: SEQ2-49N-51T  
Perfect score: 875  
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRLN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	863	98.6	166	4	US-09-397-992A-7
2	863	98.6	166	6	5514567-4
3	863	98.6	187	4	US-09-206-903A-9
4	863	98.6	187	4	US-08-406-030A-30
5	863	98.6	187	4	US-09-202-122-9
6	863	98.6	187	4	US-09-206-935-7
7	863	98.6	187	4	US-09-206-936-7
8	863	98.6	187	6	5514567-1
9	861	98.4	166	2	US-08-477-310A-1
10	858	98.1	166	1	US-08-213-448-1
11	858	98.1	166	3	US-08-912-768-1
12	858	98.1	166	5	PCT-US95-03206-1
13	858	98.1	187	3	US-08-912-768-3
14	855	97.7	187	1	US-08-026-758-22
15	846	96.7	187	6	5326859-1
16	813	92.9	187	6	5510472-6
17	803	91.8	166	1	US-08-362-453-16
18	561	64.1	187	1	US-08-026-758-21
19	481.5	55.0	186	1	US-08-026-758-25
20	451.5	51.6	186	1	US-08-026-758-26
21	429.5	49.1	186	1	US-08-026-758-24
22	363.5	41.5	186	1	US-08-026-758-23
23	257.5	29.4	208	4	US-09-397-992A-5
24	253.5	29.0	192	4	US-09-397-992A-27
25	253.5	29.0	193	4	US-09-397-992A-26
26	253.5	29.0	193	4	US-09-397-992A-29
27	253.5	29.0	208	4	US-09-206-903A-1

28	253.5	29.0	208	4	US-09-202-122-1	Sequence 1, Appli
29	253.5	29.0	208	4	US-09-206-935-1	Sequence 1, Appli
30	253.5	29.0	208	4	US-09-397-992A-2	Sequence 2, Appli
31	252	28.8	166	3	US-08-819-238A-13	Sequence 13, Appli
32	249.5	28.5	166	4	US-09-339-913B-86	Sequence 86, Appli
33	249.5	28.5	166	4	US-09-339-904A-86	Sequence 86, Appli
34	249.5	28.5	166	4	US-08-769-062B-86	Sequence 86, Appli
35	249.5	28.5	166	4	US-09-344-002B-86	Sequence 86, Appli
36	249.5	28.5	189	4	US-09-206-935-17	Sequence 17, Appli
37	249.5	28.5	189	4	US-09-206-936-17	Sequence 17, Appli
38	249	28.5	166	3	US-08-819-238A-1	Sequence 1, Appli
39	247	28.2	166	2	US-08-631-328-55	Sequence 55, Appli
40	245.5	28.1	165	1	US-08-249-671A-5	Sequence 5, Appli
41	245.5	28.1	188	1	US-08-249-671A-11	Sequence 11, Appli
42	244.5	27.9	165	1	US-08-024-330-1	Sequence 1, Appli
43	244.5	27.9	165	1	US-07-952-840-1	Sequence 1, Appli
44	244.5	27.9	165	1	US-08-356-021-1	Sequence 1, Appli
45	244.5	27.9	165	5	PCT-US94-01729-1	Sequence 1, Appli

ALIGNMENTS

```
RESULT 1
US-09-397-992A-7
; Sequence 7, Application US/09397992A
; Patent No. 6329175
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell
; APPLICANT: Grant, Francis J.
; APPLICANT: Rixon, Mark W.
; APPLICANT: Kindsvogel, Wayne
; TITLE OF INVENTION: Interferon-epsilon
; FILE REFERENCE: 98-46
; CURRENT APPLICATION NUMBER: US/09/397,992A
; CURRENT FILING DATE: 1999-09-16
; PRIOR APPLICATION NUMBER: 60/101,012
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/118,578
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/142,766
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-992A-7
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Query Match 98.6%; Score 863; DB 4; Length 166;  
Best Local Similarity 98.8%; Pred. No. 7.3e-83;  
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQNFKEAALTIY	60
Db	1	MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQNFKEAALTIY	60
QY	61	EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL	120
Db	61	EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL	120
QY	121	HLKRYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRLN	166
Db	121	HLKRYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRLN	166

RESULT 2  
5514567-4  
; Patent No. 5514567  
; APPLICANT: SUGANO, HARUO; MURAMATSU, MASAMI; TANIGUCHI,  
; TADATSUGU

```

; TITLE OF INVENTION: DNA AND RECOMBINANT PLASMID
;
; NUMBER OF SEQUENCES: 5
;
; CURRENT APPLICATION DATA:
;
;   APPLICATION NUMBER: US/08/400,179
;   FILING DATE: 06-MAR-1995
;
; PRIOR APPLICATION DATA:
;
;   APPLICATION NUMBER: 389,922
;   FILING DATE: 18-JUN-1982
;
;   APPLICATION NUMBER: 201,359
;   FILING DATE: 27-OCT-1980
;
; SEQ ID NO:4:
;   LENGTH: 166
;
5514567-4

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Query Match          98.6%; Score 863; DB 6; Length 166;
Best Local Similarity 98.8%;
Pred. NO. 7.3e-83;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 MSYNLLGELQRSSNFQCQKLLWLQNGRLEYCLKDRMNFDIPEEIKQLQnFtKEDAALTY 60

Db 1 MSYNLLGFLQRRSSNFQCCKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQOQFQKEDAAALTY 60

QY 61 EMLQNI FAIRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120

db 61 EMLQNI FAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDETRGKLMSSL 120

QY 121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGyLRN 166

Db 121 HLKRYYGRILHLYLKAKEYSHCAWTIVRVEILRNFFYNRITGYLRN 166

## RESULT 3

US-09-206-903A-9  
; Sequence 9, Application US/09206903A

; PATENT NO. 0200780  
; GENERAL INFORMATION:

APPLICANT: Chen, Jian

; APPLICANT: Godowski, Paul J.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Dong-Xiao

; TITLE OF INVENTION: NOVEL TYPE I INTERFERONS

**; FILE REFERENCE: P1224-2R1**

; CURRENT APPLICATION NUMBER: US/09/206,903A

; CURRENT FILING DATE: 1998-12-07

; PRIOR APPLICATION NUMBER: US 60/106,463

; PRIOR FILING DATE: 1998-10-30

;	NUMBER OF SEQ	ID NOS:	12
;	NUMBER OF SEQ	ID NOS:	12

; SEQ ID NO 9

; LENGTH: 187

TYPE: PRT

ORGANISM: Homo sapiens

US-09-206-903A-9

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Query Match          98.6%;   Score 863;   DB 4;   Length 187;
Best Local Similarity 98.8%;   Pred. NO. 8.5e-83;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 MSYNLLGF LQRSSNFQC KLLWQLNGRLEYCLKDRMNF DIPEEIKQLQnFtKEDAALTY 60

db 22 MSYNLLGFLQRSSNFQCCKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQFQKEDAAITY 81

QY 61 EMLQNI FAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDEFTRGKLMSSL 120

db 82 EMLQNI FAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDEFTRGKLMSSL 1411

QY 121 HLKRYYGRIHLHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166

Db 142 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNEYFINRLTGYLEN 187

## RESULT 4

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US-08-406-030A-30
; Sequence 30, Application US/08406030A
; Patent No. 6270989
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Hauge, Brian M.
; APPLICANT: Selden, Richard F
; TITLE OF INVENTION: Protein Production and Delivery
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,030A
; FILING DATE: 17-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/243,391
; FILING DATE: 13-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/985,586
; FILING DATE: 03-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,533
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,840
; FILING DATE: 05-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,188
; FILING DATE: 05-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11704
; FILING DATE: 02-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09627
; FILING DATE: 05-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: TKT95-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-406-030A-30

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Query Match          98.6%; Score 863; DB 4; Length 187;
Best Local Similarity 98.8%; Pred. NO. 8.5e-83;
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMFDIPEEIKOLQnFKEDAALTY 60

Db 22 MSYNLLGFLQRSSNFQCOKLLWQLNGRLEYCLKDRMNFDPPEIKOLOOFKEDAAALTY 81

QY 61 EMLQNI FAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120

Matches	164;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
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QY	1	MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDP	EEIKQLQnFtKEDAALTY	60
Db	22	MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDP	EEIKQLQFQKEDAALTY	81
QY	61	EMLQNIFAIFRDSSSTGWN	ETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL	120
Db	82	EMLQNIFAIFRDSSSTGWN	ETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL	141
QY	121	HLKRYYGRIHLHYLKAKEYSHCAWTIVRVEILRN	FYFINRLTGYLNRN	166
Db	142	HLKRYYGRIHLHYLKAKEYSHCAWTIVRVEILRN	FYFINRLTGYLNRN	187

  

RESULT	7
US-09-206-936-7	
;	Sequence 7, Application US/09206936A
;	Patent No. 6300475
;	GENERAL INFORMATION:
;	APPLICANT: Chen, Jian
;	APPLICANT: Wood, William I.
;	TITLE OF INVENTION: No. 6300475el Inteferon
;	FILE REFERENCE: P1224R1
;	CURRENT APPLICATION NUMBER: US/09/206,936A
;	CURRENT FILING DATE: 1998-12-07
;	EARLIER APPLICATION NUMBER: US 60/067,897
;	EARLIER FILING DATE: 1998-12-08
;	NUMBER OF SEQ ID NOS: 22
;	SEQ ID NO 7
;	LENGTH: 187
;	TYPE: PRT
;	ORGANISM: Homo sapiens
US-09-206-936-7	

  

Query Match	98.6%;	Score	863;	DB 4:	Length	187;			
Best Local Similarity	98.8%;	Pred.	No. 8.5e-83;						
Matches	164;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;

  

QY	1	MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDP	EEIKQLQnFtKEDAALTY	60
Db	22	MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDP	EEIKQLQFQKEDAALTY	81
QY	61	EMLQNIFAIFRDSSSTGWN	ETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL	120
Db	82	EMLQNIFAIFRDSSSTGWN	ETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL	141
QY	121	HLKRYYGRIHLHYLKAKEYSHCAWTIVRVEILRN	FYFINRLTGYLNRN	166
Db	142	HLKRYYGRIHLHYLKAKEYSHCAWTIVRVEILRN	FYFINRLTGYLNRN	187

  

RESULT	8
5514567-1	
;	Patent No. 5514567
;	APPLICANT: SUGANO, HARUO;MURAMATSU, MASAMI;TANIGUCHI,
;	TADATSUGU
;	TITLE OF INVENTION: DNA AND RECOMBINANT PLASMID
;	NUMBER OF SEQUENCES: 5
;	CURRENT APPLICATION DATA:
;	APPLICATION NUMBER: US/08/400,179
;	FILING DATE: 06-MAR-1995
;	PRIOR APPLICATION DATA:
;	APPLICATION NUMBER: 389,922
;	FILING DATE: 18-JUN-1982
;	APPLICATION NUMBER: 201,359
;	FILING DATE: 27-OCT-1980
;	SEQ ID NO:1:
;	LENGTH: 187
5514567-1	





; APPLICANT: Goelz, Susan E
; APPLICANT: Cate, Richard L
; APPLICANT: Pepinsky, Blake R
; APPLICANT: Chow, Pingchang E
; TITLE OF INVENTION: No. 6127332el Muteins Of IFN-Beta
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr.
; STREET: Fish & Neave, 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,768
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/475,774
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-912-768-1

Query Match 98.1%; Score 858; DB 3; Length 166;
Best Local Similarity 98.2%; Pred. No. 2.4e-82;
Matches 163; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDPPEEIKQLQNFtKEDAAITIIY 60
Db 1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDPPEEIKQLQNFQKEDAAITIIY 60

QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
Db 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120

QY 121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNPFYFINRLTGYLRN 166
Db 121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNPFYFINRLTGYLRN 166

RESULT 12
PCT-US95-03206-1
; Sequence 1, Application PC/TUS9503206
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Goelz, Susan E
; APPLICANT: Cate, Richard L
; APPLICANT: Pepinsky, Blake R
; APPLICANT: Chow, Pingchang E
; TITLE OF INVENTION: Novel Muteins Of IFN-Beta
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr.
; STREET: Fish & Neave, 1251 Avenue of the
; STREET: Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03206
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PCT-US95-03206-1

Query Match 98.1%; Score 858; DB 5; Length 166;
Best Local Similarity 98.2%; Pred. No. 2.4e-82;
Matches 163; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDPPEEIKQLQNFtKEDAAITIIY 60
Db 1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDPPEEIKQLQNFQKEDAAITIIY 60

QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
Db 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120

QY 121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNPFYFINRLTGYLRN 166
Db 121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNPFYFINRLTGYLRN 166

RESULT 13
US-08-912-768-3
; Sequence 3, Application US/08912768
; Patent No. 6127332
; GENERAL INFORMATION:
; APPLICANT: Goelz, Susan E
; APPLICANT: Cate, Richard L
; APPLICANT: Pepinsky, Blake R
; APPLICANT: Chow, Pingchang E
; TITLE OF INVENTION: No. 6127332el Muteins Of IFN-Beta
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr.
; STREET: Fish & Neave, 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: US/08/912,768  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/475,774  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B179  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 187 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-912-768-3

Query Match 98.1%; Score 858; DB 3; Length 187;  
Best Local Similarity 98.2%; Pred. No. 2.8e-82;  
Matches 163; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSYNLLGFLQSSNFQCCKLLWQLNGRLEYCLKDRMNFDPPEIKQLQnFtKEDAALTIY 60  
Db 22 MSYNLLGFLQSSNFQCCKLLWQLNGRLEYCLKDRMNFDPPEIKQLQnFtKEDAALTIY 81  
QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120  
Db 82 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 141  
QY 121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFFINRLTGYLNR 166  
Db 142 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFFINRLTGYLNR 187

RESULT 14  
US-08-026-758-22  
Sequence 22, Application US/08026758  
Patent No. 5780021  
GENERAL INFORMATION:  
APPLICANT: SOBEL, DOUGLAS O.  
TITLE OF INVENTION: A METHOD FOR TREATING AUTOIMMUNE  
DISEASES USING ALPHA-INTERFERON AND/OR BETA-INTERFERON  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 S. Jefferson Davis Highway, Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/026,758  
FILING DATE: 19930305  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Oblon, No. 5780021man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 1126-096-0  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 187 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 22..187  
OTHER INFORMATION: /note= "Hu-IFN-beta"  
US-08-026-758-22

Query Match 97.7%; Score 855; DB 1; Length 187;  
Best Local Similarity 98.2%; Pred. No. 5.9e-82;  
Matches 163; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSYNLLGFLQSSNFQCCKLLWQLNGRLEYCLKDRMNFDPPEIKQLQnFtKEDAALTIY 60  
Db 22 MSYNLLGFLQSSNFQCCKLLWQLNGRLEYCLKDRMNFDPPEIKQLQnFtKEDAALTIY 81  
QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120  
Db 82 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 141  
QY 121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFFINRLTGYLNR 166  
Db 142 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFFINRLTGYLNR 187

RESULT 15  
5326859-1  
Patent No. 5326859  
APPLICANT: Sugano, Haruo; Muramatsu, Masami; Taniguchi, Tadatsugu  
TITLE OF INVENTION: DNA AND RECOMBINANT PLASMID  
NUMBER OF SEQUENCES: 3  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/06/201,359  
FILING DATE: 27-OCT-1980  
SEQ ID NO: 1:  
LENGTH: 187  
5326859-1

Query Match 96.7%; Score 846; DB 6; Length 187;  
Best Local Similarity 97.0%; Pred. No. 5.1e-81;  
Matches 161; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSYNLLGFLQSSNFQCCKLLWQLNGRLEYCLKDRMNFDPPEIKQLQnFtKEDAALTIY 60  
Db 22 MSYNLLGFLQSSNFQCCKLLWQLNGRLEYCLKDRMNFDPPEIKQLQnFtKEDAALTIY 81  
QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120  
Db 82 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 141  
QY 121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFFINRLTGYLNR 166  
Db 142 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFFINRLTGYLNR 187

Search completed: July 29, 2002, 15:43:22  
Job time: 223 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 29, 2002, 15:39:04 ; Search time 51.64 Seconds  
(without alignments)  
357.054 Million cell updates/sec

Title: SEQ2-49N-51S  
Perfect score: 874  
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFNRLTGYLRN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:\*  
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6: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:\*  
7: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:\*  
8: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:\*  
9: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:\*  
10: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:\*  
11: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:\*  
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13: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:\*  
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15: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:\*  
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17: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:\*  
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20: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:\*  
21: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:\*  
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	870	99.5	166	22 AAU00119	Human interferon b
2	864	98.9	166	4 AAP30219	Sequence of interf
3	864	98.9	166	6 AAP50262	Sequence encoded b
4	864	98.9	166	6 AAP50279	Protein sequence e
5	864	98.9	166	7 AAP61071	Oxidation resistan
6	864	98.9	166	8 AAP70296	Sequence of interf
7	864	98.9	166	19 AAW81774	Human native inter
8	864	98.9	166	22 AAEL10346	Mature human beta-
9	864	98.9	166	22 AAEL1979	Human wild-type in
10	864	98.9	166	22 AAU00038	Human interferon b
11	864	98.9	166	22 AAU00074	Human interferon b

12	864	98.9	166	22 AAB49356	Human INF-beta A-c
13	864	98.9	166	22 AAB49357	Human INF-beta B-c
14	864	98.9	177	6 AAP50261	Sequence of beta-i
15	864	98.9	183	21 AAY84920	Amino acid sequenc
16	864	98.9	183	21 AAY70866	Histidine tagged-h
17	864	98.9	187	2 AAP10016	Sequence of fibrob
18	864	98.9	187	3 AAP20026	Human fibroblast i
19	864	98.9	187	15 AAR56987	Human fibroblast i
20	864	98.9	187	19 AAW61154	Human interferon b
21	864	98.9	187	20 AAY05380	Human HCMV inducib
22	864	98.9	187	22 AAE10345	Human beta-interfe
23	864	98.9	187	22 AAB49776	Human interferon b
24	864	98.9	399	21 AAY70867	Human interferon-b
25	864	98.9	415	20 AAY25371	IFNAR2/IFN-beta co
26	863	98.7	166	7 AAP60687	Sequence between t
27	862	98.6	166	22 AAU00103	Human interferon b
28	862	98.6	166	22 AAU00150	Human interferon b
29	861	98.5	166	22 AAU00070	Human interferon b
30	861	98.5	166	22 AAU00072	Human interferon b
31	861	98.5	166	22 AAU00075	Human interferon b
32	861	98.5	166	22 AAU00083	Human interferon b
33	861	98.5	166	22 AAU00085	Human interferon b
34	861	98.5	166	22 AAU00124	Human interferon b
35	861	98.5	166	22 AAU00143	Human interferon b
36	861	98.5	166	22 AAU00159	Human interferon b
37	861	98.5	166	22 AAU00160	Human interferon b
38	861	98.5	187	3 AAP20049	Interferon-beta ge
39	860	98.4	166	22 AAU00073	Human interferon b
40	860	98.4	166	22 AAU00077	Human interferon b
41	860	98.4	166	22 AAU00078	Human interferon b
42	859	98.3	165	22 AAU00139	Human interferon b
43	859	98.3	166	6 AAP50197	Modified human int
44	859	98.3	166	16 AAR82607	IFN-beta(Phe101).
45	859	98.3	166	22 AAU00079	Human interferon b

ALIGNMENTS

RESULT 1	
AAU00119	
ID	AAU00119 standard; Protein; 166 AA.
XX	
AC	AAU00119;
XX	
DT	16-MAY-2001 (first entry)
XX	
DE	Human interferon beta mutant Q49N/Q51T.
XX	
KW	Human; interferon beta; antibody; multiple sclerosis; gene therapy;
KW	viral infection; viral hepatitis; cancer; breast cancer; inflammation;
KW	Crohn's disease; acute myeloid leukaemia; Hodgkin's disease;
KW	ulcerative colitis; immunomodulation; mutant; mutein; Q49N/Q51T.
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 49
FT	/note= "Wild-type Gln replaced with Asn"
FT	Misc-difference 51
FT	/note= "Wild-type Gln replaced with Thr"
XX	
PN	WO200115736-A2.
XX	
PD	08-MAR-2001.
XX	
PF	25-AUG-2000; 2000WO-DK00471.
XX	
PR	27-AUG-1999; 99DK-0001197.
PR	21-OCT-1999; 99US-0160782.
PR	26-NOV-1999; 99DK-0001691.
PR	07-FEB-2000; 2000DK-0000194.
PR	07-MAR-2000; 2000DK-0000363.

PR 14-APR-2000; 2000DK-0000642.  
XX (MAXY-) MAXYGEN APS.  
PA Pedersen AH, Schambye HT, Andersen KV, Bornaes C, Rasmussen PB;  
XX WPI; 2001-218488/22.  
XX A conjugate exhibiting interferon beta activity useful for treating  
PT multiple sclerosis comprises a non-polypeptide group covalently  
PT attached to an interferon beta polypeptide -  
XX  
PS Claim 39; Page - ; 108pp; English.  
XX  
CC The sequence represents Human interferon beta mutant Q49N/Q51T.  
CC Conjugates of the invention exhibiting interferon beta activity  
CC comprise at least one first non-polypeptide group covalently attached  
CC to an interferon beta polypeptide, the amino acid sequence of which  
CC differs from wild-type human interferon beta in at least one introduced  
CC and at least one removed amino acid residue comprising an attachment  
CC group for the first non-polypeptide group. The invention also concerns  
CC reducing the immunogenicity and/or increasing functional in vivo  
CC half-life and/or serum half-life of an interferon beta polypeptide  
CC comprising introducing an amino acid residue constituting an attachment  
CC group for a first non-polypeptide group into a position exposed at the  
CC surface of the protein that does not contain such a group and removing  
CC an amino acid residue constituting an attachment group for a first  
CC non-polypeptide group and subjecting the modified peptide to conjugation  
CC with the non-polypeptide group. The conjugate and a cell culture  
CC expressing the mutated polypeptides are useful in the treatment of  
CC disease, especially multiple sclerosis, and for treating mammals having  
CC circulating antibodies against interferon beta 1a or 1b. DNA encoding the  
CC mutated proteins may be used for gene therapy. The DNA and proteins can  
CC also be used to treat viral infections (e.g viral hepatitis), cancer  
CC (e.g. breast cancer), inflammation, Crohn's disease, acute myeloid  
CC leukaemia, Hodgkin's disease and ulcerative colitis and for  
CC immunomodulation.  
CC Note: The present sequence is not shown in the specification but is  
CC derived from the human interferon beta sequence given in AAU00038.  
XX  
SQ Sequence 166 AA;

Query Match 99.5%; Score 870; DB 22; Length 166;  
Best Local Similarity 99.4%; Pred. No. 4.4e-68;  
Matches 165; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MSYNLLGLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDPPEIKQLQnFsKEDAALTIY 60  
Db 1 msynllglqrssnfgqkllwqlngrleyclckdrnmfdipeeikqlnqfkedaaltiy 60  
QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120  
Db 61 emlqnifaifrqsdsstgwnetivenllanvyhqinhkltvleeklekedftrgklmssl 120  
QY 121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGyLRN 166  
Db 121 hlkryygrilhyllkakeyshcawtivrveilrnfyfnrltgyln 166

RESULT 2  
AAP30219  
ID AAP30219 standard; Protein; 166 AA.  
XX  
AC AAP30219;  
XX  
DT 25-MAY-1992 (first entry)  
XX  
DE Sequence of Interferon (HuIFN) -beta-1 encoded by plasmid  
DE PDM101/trp/beta-1.  
XX  
KW Hybrid interferon; antiviral; therapy; cancer; tumour.

OS Homo sapiens.  
XX  
PN WO8302461-A.  
XX  
PD 21-JUL-1983.  
XX  
PF 18-JAN-1983; 83WO-0900607.  
XX  
PR 19-JAN-1982; 82US-0340782.  
PR 03-FEB-1983; 83US-0463574.  
PR 15-JUL-1985; 85US-0755265.  
XX  
PA (CETU-) CETUS CORP.  
XX  
PI Mark DF, Creasey AA;  
XX WPI; 1983-723186/30.  
DR N-PSDB; AAN30152.  
DR  
XX  
PT Multi-class hybrid interferon poly:peptide(s) - with restricted  
PT antiviral and cell growth regulatory activities  
XX  
PS Example; Fig 5; 61pp; English.  
XX  
CC The inventors claim a multiclass hybrid interferon polypeptide and a  
CC DNA unit having a nucleotide sequence which encodes it. Pref. the  
CC AA sequence consists of alpha and beta interferons. Pref. IF1 is  
CC (i) the 1-73 AA seq. of HuIFN-alpha-1 (and IF2 is the 74-166 AA seq.  
CC of HuIFN-beta-1) (see AAN30155, AAP30222); or (ii) the 1-41 AA seq. of  
CC HuIFN-alpha-61A (and IF2 is the 43-166 AA seq. of HuIFN-beta-1) (see  
CC AAN30160, AAP30227). Alternatively IF1 is the amino terminal end of a  
CC beta-IF and IF2 is the carboxy terminal of an alpha-IF (esp. the  
CC 1-73 seq. of HuIFN-beta-1 and the 74-167 seq. of HuIFN-alpha-1  
CC resp.) (see AAN30156, AAP30223). In the examples plasmids PGW5 and  
CC PDM101/trp/beta-1 and p-alpha-61A were used (see AAN30151, AAN30152,  
CC AAN30157). HinfI was used to digest the DNA sequences in the region  
CC of significant handicaps (see AAN30153, AAN30154, AAN30158, AAN30159),  
CC and the restriction fragments were ligated to form hybrid DNA.  
XX  
SQ Sequence 166 AA;

Query Match 98.9%; Score 864; DB 4; Length 166;  
Best Local Similarity 98.8%; Pred. No. 1.5e-67;  
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MSYNLLGLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDPPEIKQLQnFsKEDAALTIY 60  
Db 1 msynllglqrssnfgqkllwqlngrleyclckdrnmfdipeeikqlnqfkedaaltiy 60  
QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120  
Db 61 emlqnifaifrqsdsstgwnetivenllanvyhqinhkltvleeklekedftrgklmssl 120  
QY 121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGyLRN 166  
Db 121 hlkryygrilhyllkakeyshcawtivrveilrnfyfnrltgyln 166

RESULT 3  
AAP50262  
ID AAP50262 standard; Protein; 166 AA.  
XX  
AC AAP50262;  
XX  
DT 20-NOV-1991 (first entry)  
XX  
DE Sequence encoded by the sequence between the EcoRI site and the  
DE xhoII site of p-beta-1-trp.  
XX  
KW Expression vector; trp promoter-operator; transformed bacteria.  
XX  
PN US4499188-A.









Best Local Similarity 98.8%; Pred. No. 1.5e-67;  
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLLGFLQRSSNFQCCKLLWQLNGRLEYCLKDRMFDPBEIKQLQNFSKEDAAALTIY 60  
|||||  
Db 1 msynllgflqrssnfcqkllwqlngrleyclckdrmfdpbeelqqlqfkedaalty 60

QY 61 EMLQNIFAIFRODSSSTGWNETIVENLLANVYHQINHLKTIVLEEKLEKEDEFTRGKLMSL 120  
61 emlqnifairqdssstgwnetivenllanvyhqinhiktvleeklekedftrgklmssl 120

QY 121 HLKRYYGRIILHYLKAKESHCWATIVRVEILRNIFYFINRLTGYLNRN 166  
121 hlkryygrilhlhylkakeyshcawtivrveillrnfyfinrltgylrn 166

RESULT 10  
AAU00038  
ID AAU00038 standard; Protein; 166 AA.  
XX  
AC AAU00038;  
XX  
DT 16-MAY-2001 (first entry)  
XX  
DE Human interferon beta.  
XX  
KW Human; interferon beta; antibody; multiple sclerosis; gene therapy;  
KW viral infection; viral hepatitis; cancer; breast cancer; inflammation;  
KW Crohn's disease; acute myeloid leukaemia; Hodgkin's disease;  
KW ulcerative colitis; immunomodulation.  
XX  
OS Homo sapiens.  
XX  
PN WO200115736-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 25-AUG-2000; 2000WO-DK00471.  
XX  
PR 27-AUG-1999; 99DK-0001197.  
PR 21-OCT-1999; 99US-0160782.  
PR 26-NOV-1999; 99DK-0001691.  
PR 07-FEB-2000; 2000DK-0000194.  
PR 07-MAR-2000; 2000DK-0000363.  
PR 14-APR-2000; 2000DK-0000642.  
XX  
PA (MAXY-) MAXYGEN APS.  
XX  
PI Pedersen AH, Schambye HT, Andersen KV, Bornaes C, Rasmussen PB;  
XX  
DR WPI; 2001-218488/22.  
DR N-PSDB; AAS00067.  
XX  
PT A conjugate exhibiting interferon beta activity useful for treating  
PT multiple sclerosis comprises a non-polypeptide group covalently  
PT attached to an interferon beta polypeptide -  
XX  
PS Example 1; Page 99-100; 108pp; English.  
XX  
CC The sequence is Human interferon beta. Conjugates of the invention  
CC exhibiting interferon beta activity comprise at least one first  
CC non-polypeptide group covalently attached to an interferon beta  
CC polypeptide, the amino acid sequence of which differs from wild-type  
CC human interferon beta in at least one introduced and at least one removed  
CC amino acid residue comprising an attachment group for the first  
CC non-polypeptide group. The invention also concerns reducing the  
CC immunogenicity and/or increasing functional in vivo half-life and/or  
CC serum half-life of an interferon beta polypeptide comprising introducing  
CC an amino acid residue constituting an attachment group for a first  
CC non-polypeptide group into a position exposed at the surface of the  
CC protein that does not contain such a group and removing an amino acid  
CC residue constituting an attachment peptide to conjugation with the  
CC group and subjecting the modified peptide to conjugation with the







PT diseases -

XX

PS Example 1; Fig 10; 73pp; English.

XX

The present sequence represents a His-tagged Interferon beta la (IFN-beta la) protein. The protein is used to produce a composition comprising a glycosylated IFN-beta coupled to a non-naturally-occurring polymer containing a polyalkylene glycol. The composition has enhanced activity, measured by an antiviral assay, as compared to physiologically active IFN-beta. The polymer-IFN-beta conjugate has the ability to stay in the vasculature for longer periods of time, has increased stability in solution, reduced immunogenicity, protection of the modified IFN-beta-la from proteolytic digestion and subsequent abolition activity, and increased thermal stability. The polymer-based conjugates are useful for treating tumors and cancer, as well as autoimmune conditions such as fibrosis, lupus and multiple sclerosis. These may also be used in the treatment of viral diseases, as well as in the treatment of angiogenic diseases. IFN-beta la is useful as an agent for the treatment, remission or attenuation of a disease state, physiological condition, symptoms or etiological factors, or for their evaluation or diagnosis. The IFN-beta la polymer conjugates may also be used for prophylaxis or treatment of any condition or disease state for which the IFN-beta la constituent is efficacious, in biological systems or specimens.

XX

**SQ Sequence 183 AA;**

Query Match 98.9%; Score 864; DB 21; Length 183;

Best Local Similarity 98.8%; Pred. No. 1.6e-67;

**Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;**

QY 1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDPPEEIKQLQnFSKEDAALTY 60

Db 18 msynllgflqrsnfcqckllwqlngrleyclldrmnfdipeelkqlqgfkedaaltiy 77

QY 61 EMLQNI FAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120

Db  
78 emlqn1faifrqdsstgwnetivenllanvyhqinhkvtyleekedftrgklmssl 137

QY 121 HLKRYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRLN 166

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Db
138 hlkryygrilhyllkakeyshcawtivrveillnfyfinrltgyln 183
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Search completed: July 29, 2002, 15:42:54

Job time: 230 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 29, 2002, 15:41:34 ; Search time 46.62 Seconds  
(without alignments)  
615.984 Million cell updates/sec

Title: SEQ2-49N-51S  
Perfect score: 874  
Sequence: 1 MSYNLLGLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRLN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phage:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_rvirus:\*
  - 16: sp\_bacteriap:\*
  - 17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	822	94.1	187	6 077812	077812 macaca fasc
2	817	93.5	187	4 Q15943	Q15943 homo sapien
3	525.5	60.1	186	6 Q29412	Q29412 sus scrofa
4	255.5	29.2	195	6 Q9GLL5	Q9GLL5 bos taurus
5	250.5	28.7	189	4 Q14618	Q14618 homo sapien
6	245.5	28.1	188	4 Q96KI6	Q96KI6 homo sapien
7	245	28.0	195	6 Q28844	Q28844 oryctolagus
8	244	27.9	189	6 Q95J78	Q95J78 saguinus oe
9	242	27.7	189	6 Q95J77	Q95J77 saguinus oe
10	241.5	27.6	189	4 Q14607	Q14607 homo sapien
11	239.5	27.4	195	6 Q9GLL6	Q9GLL6 bos taurus
12	237	27.1	174	4 Q13168	Q13168 homo sapien
13	237	27.1	195	6 Q28845	Q28845 oryctolagus
14	237	27.1	195	6 Q28562	Q28562 ovis aries
15	237	27.1	195	6 Q28545	Q28545 ovis aries
16	236.5	27.1	189	4 Q14639	Q14639 homo sapien

17	236.5	27.1	195	6 Q9MYK6	Q9myk6 bos taurus
18	236.5	27.1	195	6 Q95NE2	Q95ne2 bos taurus
19	235	26.9	195	6 Q28843	Q28843 oryctolagus
20	235	26.9	195	6 Q28847	Q28847 oryctolagus
21	235	26.9	195	6 Q28561	Q28561 ovis aries
22	226	25.9	190	6 Q29085	Q29085 sus scrofa
23	225.5	25.8	179	6 Q29084	Q29084 sus scrofa
24	223.5	25.6	195	6 P28170	P28170 ovis aries
25	221.5	25.3	181	4 Q14608	Q14608 homo sapien
26	220	25.2	190	6 Q29098	Q29098 sus scrofa
27	219	25.1	190	11 Q9ES91	Q9es91 marmota mon
28	218	24.9	166	4 Q9UMJ3	Q9umj3 homo sapien
29	218	24.9	189	4 Q14605	Q14605 homo sapien
30	215.5	24.7	207	4 Q9P0W0	Q9p0w0 homo sapien
31	213	24.4	190	11 Q61719	Q61719 mus musculu
32	209	23.9	190	11 Q99N22	Q99n22 marmota mon
33	201	23.0	190	11 Q64138	Q64138 cricetinae
34	198	22.7	84	6 Q95LB8	Q95lb8 sus scrofa
35	195.5	22.4	170	6 Q29114	Q29114 sus scrofa
36	194	22.2	190	11 Q61718	Q61718 mus musculu
37	194	22.2	190	11 Q91WX3	Q91wx3 sigmodon hi
38	193.5	22.1	170	6 Q29115	Q29115 sus scrofa
39	188	21.5	108	6 Q9N1U6	Q9nlu6 equus cabal
40	187	21.4	166	6 P79228	P79228 odocoileus
41	186	21.3	190	11 Q61716	Q61716 mus musculu
42	181	20.7	136	11 Q61717	Q61717 mus musculu
43	148.5	17.0	193	13 Q9PWI5	Q9pwi5 gallus gall
44	146.5	16.8	182	11 Q9R1T0	Q9r1t0 mus musculu
45	132.5	15.2	193	13 Q9PWI6	Q9pwi6 gallus gall

ALIGNMENTS

RESULT	1
O77812	
ID	O77812 PRELIMINARY; PRT; 187 AA.
AC	O77812;
DT	01-NOV-1998 (Tremblrel. 08, Created)
DT	01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE	INTERFERON BETA.
GN	IFN-BETA.
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC	Cercopithecinæ; Macaca.
OX	NCBI_TaxID=9541;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=99156140; PubMed=10048395;
RA	Matheux F., Le Grand R., Rousseau V., De Maeyer E., Dormont D.,
RA	Lauret E.;
RT	"Macaque lymphocytes transduced by a constitutively expressed
RT	interferon beta gene display an enhanced resistance to SIVmac251
RT	infection."
RL	Hum. Gene Ther. 10:429-429(1999).
CC	-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC	FAMILY.
DR	EMBL; AJ011909; CAA09862.1; -.
DR	HSSP; P01574; 1AU1.
DR	InterPro; IPR000471; Interferon_abd.
DR	Pfam; PF00143; interferon; 1.
DR	PRINTS; PR00266; INTERFERONAB.
DR	ProDom; PD000550; Interferon_abd; 1.
DR	SMART; SM00076; IFabd; 1.
DR	PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW	Antiviral; Cytokine.
SQ	SEQUENCE 187 AA; 22266 MW; 376AEF7332B7807 CRC64;

Query Match 94.1%; Score 822; DB 6; Length 187;  
Best Local Similarity 92.8%; Pred. No. 2e-63;





DR	EMBL; AF238613; AAG14170.1; -.				
DR	HSSP; P01563; 2HIE.				
DR	InterPro; IPR000471; Interferon_abd.				
DR	Pfam; PF00143; Interferon; 1.				
DR	PRINTS; PR00266; INTERFERONAB.				
DR	ProDom; PD000550; Interferon_abd; 1.				
DR	SMART; SM00076; IFabd; 1.				
DR	PROSITE; PS00252; INTERFERON_A_B_D; 1.				
KW	Antiviral; Cytokine.				
SQ	SEQUENCE 195 AA; 22139 MW; 689C2443B203E50A CRC64;				
Query Match 29.2%; Score 255.5; DB 6; Length 195;					
Best Local Similarity 39.0%; Pred. No. 1.4e-14;					
Matches 53; Conservative 30; Mismatches 50; Indels 3; Gaps 2;					
QY	19 KLLWQLNGRL--EYCLKDRMNFDP EEEIKQLQnFsKEDAAALTIYEMLQNIFAIFRQDSSS 76				
Db	39 RLLAQMN-RLSTHSCLDKRDGFLPWEMVEGDQLQKDQAISVLHEMLQQCFNLFHTEHSS 97				
QY	77 TGNWETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSSLHLKRYYGRIILHYLKAK 136				
Db	98 AAWNTTLLLEQLCTGLHQQLDDLDACLQGVMEKDSALGRMGPILTVKKYFQGIHVYLKKK 157				
QY	137 EYSHCAWTIVRVEILR 152				
Db	158 EYSDCAWEIIRVEMMR 173				
RESULT 5					
Q14618					
ID	Q14618 PRELIMINARY; PRT; 189 AA.				
AC	Q14618;				
DT	01-NOV-1996 (TrEMBLrel. 01, Created)				
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)				
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)				
DE	INTERFERON ALPHA-N.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Gren E.Y., Berzin V.M., Tsimanis A.Y., Apsalon U.R., Vishnevskii Y.I.,				
RA	Yansone I.V., Dishler A.V., Pudova N.V., Smorodintsev A.A.,				
RA	Iovlev V.I., Stepanov A.N., Feldmane G.Y., Meldrais Y.A., Lozha V.P.,				
RA	Kavsan V.M., Efimov V.A., Sverdlov E.D.;				
RT	"A new type of leukocytic interferon.";				
RL	Dokl. Biochem. 269:91-95(1983).				
CC	-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA				
CC	FAMILY.				
DR	EMBL; X00140; CAA24970.1; -.				
DR	HSSP; P01563; 2HIE.				
DR	InterPro; IPR000471; Interferon_abd.				
DR	Pfam; PF00143; Interferon; 1.				
DR	PRINTS; PR00266; INTERFERONAB.				
DR	ProDom; PD000550; Interferon_abd; 1.				
DR	SMART; SM00076; IFabd; 1.				
DR	PROSITE; PS00252; INTERFERON_A_B_D; 1.				
KW	Antiviral; Cytokine.				
SQ	SEQUENCE 189 AA; 21810 MW; E6D8D9E726E04344 CRC64;				
Query Match 28.7%; Score 250.5; DB 4; Length 189;					
Best Local Similarity 35.8%; Pred. No. 3.6e-14;					
Matches 53; Conservative 30; Mismatches 62; Indels 3; Gaps 2;					
QY	20 LLWQLNGRLEY--CLKDRMNFDP EEEIKQLQnFsKEDAAALTIYEMLQNIFAIFRQDSSST 77				
Db	40 LLAQM-GRISHFSCLDKRDYDFGFPQEVFDGNQFQKAQAISAFHEMIQQTFNLFSTKDSSA 98				
QY	78 GWNWETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSSLHLKRYYGRIILHYLKAKE 137				

Db	99 AWDETLLDKFYIELFQQLNDEACVTOEVGVVEIATMNEDSLAVRKYFORITLYLMGKK 158				
QY	138 YSHCAWTIVRVEILRNIFYFINRLTGYLRL 165				
Db	159 YSPCAWEVVRAEIMRSFSFSSTNLQKGLR 186				
RESULT 6					
Q96KI6					
ID	Q96KI6 PRELIMINARY; PRT; 188 AA.				
AC	Q96KI6;				
DT	01-DEC-2001 (TrEMBLrel. 19, Created)				
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)				
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)				
DE	INTERFERON ALPHA 2 PRECURSOR.				
GN	IFNA2.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=PLACENTA;				
RX	MEDLINE=98357449; Pubmed=9694076;				
RA	Austruy E., Bagnis C., Carbuccia N., Maroc C., Birg F., Dubreuil P.,				
RA	Mannoni P., Chabannon C.;				
RT	"A defective retroviral vector encoding human interferon alpha 2 can				
RT	transduce human leukemic cell lines.";				
RL	Cancer Gene Ther. 5:247-256(1998).				
DR	EMBL; Y11834; CAA72532.1; -. POTENTIAL.				
FT	SIGNAL 1 23				
SQ	SEQUENCE 188 AA; 21578 MW; 9BAA221D2BFB421D CRC64;				
Query Match 28.1%; Score 245.5; DB 4; Length 188;					
Best Local Similarity 35.3%; Pred. No. 9.7e-14;					
Matches 60; Conservative 26; Mismatches 53; Indels 31; Gaps 5;					
QY	5 LLGFLQRSSNFQCKLLWQLNGRLEYCLKDRMNFDP EEEIKQLQn-FsKEDAAALTIYEML 63				
Db	40 LLAQMRRLSLSF-----CLKDRHDFGFPQE--EFGNQFQKAETIPVLHEMI 83				
QY	64 QNIFAIFRQDSSSTGWNWETIVENLLANVYHQINHLKT-----VLEEKLEKEDFTRGKL 116				
Db	84 QQIFNLSTKDSSAAWDETLLDKFYELYQQNLDEACVIGVGVTETPLMKD----- 137				
QY	117 MSSHLKRYYGRIILHYLKAKEYSHCAWTIVRVEILRNIFYFINRLTGYLRLN 166				
Db	138 -SILAVRKYFORITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQESLRS 186				
RESULT 7					
Q28844					
ID	Q28844 PRELIMINARY; PRT; 195 AA.				
AC	Q28844;				
DT	01-NOV-1996 (TrEMBLrel. 01, Created)				
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)				
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)				
DE	INTERFERON-OMEGA48.				
OS	Oryctolagus cuniculus (Rabbit).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
OX	NCBI_TaxID=9986;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=94132653; Pubmed=8301151;				
RA	Charlier M., L'Haridon R., Boissnard M., Martal J., Gaye P.;				
RT	"Cloning and structural analysis of four genes encoding interferon-				
RT	omega in rabbit.";				
RL	J. Interferon Res. 13:313-322(1993).				
CC	-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA				
CC	FAMILY.				
DR	EMBL; S68999; AAC60525.2; -.				



```

01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INTERFERON OMEGA-1 (FRAGMENT).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
Zeng Q., Li M., Zhou Y., Guo H., Hou Y.;
"The cloning, sequencing of the primary structure and expression in E. coli Chinese human IFN-W1 gene.";
Sci. China B. 0:0-0(0).
[2]
SEQUENCE FROM N.A.
Xu L.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA FAMILY.
EMBL; U25670; AAA70091.1; -.
HSSP; P01563; 2HIE.
InterPro; IPR000471; Interferon_abd.
Pfam; PF00143; interferon; 1.
PRINTS; PR00266; INTERFERONAB.
ProDom; PD000550; Interferon_abd; 1.
SMART; SM00076; IFabd; 1.
PROSITE; PS00252; INTERFERON_A_B_D; 1.
Antiviral; Cytokine.
NON_TER 1
SEQUENCE 174 AA; 20249 MW; BLCC9AB5993016C5 CRC64;

Query Match      27.1%; Score 237; DB 4; Length 174;
Best Local Similarity 33.8%; Pred. No. 4.8e-13;
Matches 46; Conservative 32; Mismatches 58; Indels 0; Gaps

QY 31 CLKDRMNFDIPEEIQLQNfSKEDAALTIYEMLQNFPAIFRDSSSTGWNETIVENLLAN 90
||||| : | | : : | : ||||| ||| : | | | | : | : | : | : |
Db 31 CLKDRRRDFRPQEMVGKSQLQKAHVMSALHEMLQQIFSLEHTERSAAWNMTLLDQLHTG 90

QY 91 VYHQINHLKTIVLEEKLEKEDETRGKLMSLHLKRYIGRLHYLKAKKEYSHCAWTIVRVEI 150
:: : ||| : | : : : | | : || : | ||| : ||| : ||| : | : | : | : |
Db 91 LHQLQHLETCLLVGVGESESAGAISSPALTLRRYFQGITRVYLKEKKYSDCAWDEVDRMEI 150

QY 151 LRNFYFINRLTGYLRN 166
:: : : : || :
Db 151 MKSLFLSTNMQERLS 166

RESULT 13
Q28845 PRELIMINARY; PRT; 195 AA.
ID Q28845 AC Q28845;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERFERON-OMEGA45.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94132653; PubMed=8301151;
RA Charlier M., L'Haridon R., Boissard M., Martal J., Gaye P.;
RT "Cloning and structural analysis of four genes encoding interferon-omega in rabbit.";
RL J. Interferon Res. 13:313-322(1993).
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA FAMILY.
CC EMBL; S69000; AAC60526.1; -.
DR HSSP; P01563; 2HIE.
```





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 29, 2002, 15:42:54 ; Search time 51.64 Seconds  
(without alignments)  
357.054 Million cell updates/sec

Title: SEQ2-49N-51T

Perfect score: 875

Sequence: 1 MSYNLLGLQRSSNFQCQKL.....RVEILRNFYFINRLTGVLRN 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_032802.\*  
1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.\*  
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11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.\*  
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16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.\*  
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20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	869	99.3	166	22 AAU00119	Human interferon b
2	866	99.0	166	22 AAU00103	Human interferon b
3	866	99.0	166	22 AAU00150	Human interferon b
4	863	98.6	166	4 AAP30219	Sequence of interf
5	863	98.6	166	6 AAP50262	Sequence encoded b
6	863	98.6	166	6 AAP50279	Protein sequence e
7	863	98.6	166	7 AAP61071	Oxidation resistan
8	863	98.6	166	8 AAP70296	Sequence of interf
9	863	98.6	166	19 AAW81774	Human native inter
10	863	98.6	166	22 AAEL10346	Mature human beta-
11	863	98.6	166	22 AAEL1979	Human wild-type in

12	863	98.6	166	22 AAU00038	Human interferon b
13	863	98.6	166	22 AAU00074	Human interferon b
14	863	98.6	166	22 AAB49356	Human INF-beta A-c
15	863	98.6	166	22 AAB49357	Human INF-beta B-c
16	863	98.6	177	6 AAP50261	Sequence of beta-1
17	863	98.6	183	21 AAY84920	Amino acid sequenc
18	863	98.6	183	21 AAY70866	Histidine tagged-h
19	863	98.6	187	2 AAP10016	Sequence of fibrob
20	863	98.6	187	3 AAP20026	Human fibroblast i
21	863	98.6	187	15 AAR56987	Human fibroblast i
22	863	98.6	187	19 AAW61154	Human interferon b
23	863	98.6	187	20 AAY05380	Human HCMV inducib
24	863	98.6	187	22 AAEL10345	Human beta-interfe
25	863	98.6	187	22 AAB49776	Human interferon b
26	863	98.6	399	21 AAY70867	Human interferon-b
27	863	98.6	415	20 AAY25371	IFNAR2/IFN-beta co
28	862	98.5	166	7 AAP60687	Sequence between t
29	860	98.3	166	22 AAU00070	Human interferon b
30	860	98.3	166	22 AAU00072	Human interferon b
31	860	98.3	166	22 AAU00075	Human interferon b
32	860	98.3	166	22 AAU00083	Human interferon b
33	860	98.3	166	22 AAU00085	Human interferon b
34	860	98.3	166	22 AAU00124	Human interferon b
35	860	98.3	166	22 AAU00137	Human interferon b
36	860	98.3	166	22 AAU00143	Human interferon b
37	860	98.3	166	22 AAU00159	Human interferon b
38	860	98.3	166	22 AAU00160	Human interferon b
39	860	98.3	187	3 AAP20049	Interferon-beta ge
40	859	98.2	166	22 AAU00073	Human interferon b
41	859	98.2	166	22 AAU00077	Human interferon b
42	859	98.2	166	22 AAU00078	Human interferon b
43	858	98.1	165	22 AAU00139	Human interferon b
44	858	98.1	166	6 AAP50197	Modified human int
45	858	98.1	166	16 AAR82607	IFN-beta(Phel01) .

ALIGNMENTS

RESULT 1  
AAU00119  
ID AAU00119 standard; Protein; 166 AA.  
XX  
AC AAU00119;  
XX  
DT 16-MAY-2001 (first entry)  
XX  
DE Human interferon beta mutant Q49N/Q51T.  
XX  
KW Human; interferon beta; antibody; multiple sclerosis; gene therapy;  
KW viral infection; viral hepatitis; cancer; breast cancer; inflammation;  
KW Crohn's disease; acute myeloid leukaemia; Hodgkin's disease;  
KW ulcerative colitis; immunomodulation; mutant; mutein; Q49N/Q51T.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 49 /note= "Wild-type Gln replaced with Asn"  
FT Misc-difference 51 /note= "Wild-type Gln replaced with Thr"











Db 61 emlnqifaifrqdssstgwnetivenllanvyhqinhkltvleeklekedftrgklmssl 120

QY 121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGyLRN 166

Db 121 hlkrYYgrilhyLkakeYshCAwtIvrveILrnfYfinrltgyLrn 166

RESULT 9

AAW81774

ID AAW81774 standard; protein; 166 AA.

XX

AC AAW81774;

XX

DT 29-JAN-1999 (first entry)

XX

DE Human native interferon-beta protein.

XX

KW Interferon-Beta; variant; human; medicament; treatment; screening;

KW multiple sclerosis; measurement; water soluble.

XX

OS Homo sapiens.

XX

PN DE19717864-A1.

XX

PD 29-OCT-1998.

XX

PE 23-APR-1997; 97DE-1017864.

XX

PR 23-APR-1997; 97DE-1017864.

XX

PA (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

XX

PI Otto B, Schneider-Fresenius C, Waschuetza G;

XX

DR WPI; 1998-569784/49.

XX

PT New mutated recombinant human interferon-beta protein contains

PT hydroxylic amino acid substitutions to improve water solubility -

PT used e.g. in in vitro screening assays, to measure interferon levels

PT and to treat multiple sclerosis

XX

PS Disclosure; Fig 1; 18pp; German.

XX

CC This sequence represents a native human recombinant interferon-beta

CC protein which is mutated into an amino acid having at least one hydroxy

CC group substituted for at least one of Leu5, Phe8, Phe15, Leu47, Phe50,

CC Leu106, Phe111, Leu116, Leu120 and Phe156. Such mutants can be used in

CC medicaments e.g. for treating multiple sclerosis, for in vitro screening

CC assays and for measurement of interferon levels. The mutated protein is

CC more water-soluble than recombinant wild-type human interferon-beta.

XX

SQ Sequence 166 AA;

Query Match 98.6%; Score 863; DB 19; Length 166;

Best Local Similarity 98.8%; Pred. No. 8.2e-70;

Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLLGLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQNfTKEDAALTIY 60

Db 1 msynllgflqrssnfqcqkllwqlngrleyclckdrnmfdipeeikqlqfqkedaaltiy 60

QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHkLTvLEEKLEKEDfTRGKLmSSL 120

Db 61 emlnqifaifrqdssstgwnetivenllanvyhqinhkltvleeklekedftrgklmssl 120

QY 121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGyLRN 166

Db 121 hlkrYYgrilhyLkakeYshCAwtIvrveILrnfYfinrltgyLrn 166

RESULT 10

AAE10346

ID AAE10346 standard; Protein; 166 AA.

XX

AC AAE10346;

XX

DT 10-DEC-2001 (first entry)

XX

DE Mature human beta-interferon.

XX

KW Human; beta-interferon; INF-beta; immune disease; demyelinating disease;

KW sub-acute sclerosing panencephalomyelitis; SSPE; multiple sclerosis;

KW metachromatic leukodystrophy; Guillain-Barre syndrome;

KW autoimmune disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 162

FT /note= "Encoded by CGT"

XX

PN EP1133997-A2.

XX

PD 19-SEP-2001.

XX

PF 20-FEB-2001; 2001EP-0103580.

XX

PR 23-FEB-2000; 2000EP-0440053.

PR 07-NOV-2000; 2000US-0246089.

XX

PA (TRGE ) TRANSGENE SA.

XX

PI Braun S;

XX

DR WPI; 2001-572706/65.

DR N-PSDB; AAD17506.

XX

PT Use of nucleic acid for the treatment of immune diseases such as

PT multiple sclerosis -

XX

PS Claim 9; Page 15; 2lpp; English.

XX

CC The invention relates to use of nucleic acids expressing human

CC beta-interferon (INF-beta) for the treatment of immune diseases such as

CC demyelinating disease (e.g. sub-acute sclerosing panencephalomyelitis

CC (SSPE), metachromatic leukodystrophy, Guillain-Barre syndrome) and

CC autoimmune disease (e.g. multiple sclerosis). The expression of the

CC beta-interferon results in the improvement of the clinical status of

CC the treated mammal, thus avoiding the use of recombinant polypeptide.

CC The nucleic acid is therefore compatible with the quality of life of the

CC patients. The present sequence is mature human beta-interferon.

XX

SQ Sequence 166 AA;

Query Match 98.6%; Score 863; DB 22; Length 166;

Best Local Similarity 98.8%; Pred. No. 8.2e-70;

Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSYNLLGLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQNfTKEDAALTIY 60

Db 1 msynllgflqrssnfqcqkllwqlngrleyclckdrnmfdipeeikqlqfqkedaaltiy 60

QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHkLTvLEEKLEKEDfTRGKLmSSL 120

Db 61 emlnqifaifrqdssstgwnetivenllanvyhqinhkltvleeklekedftrgklmssl 120

QY 121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGyLRN 166

Db 121 hlkrYYgrilhyLkakeYshCAwtIvrveILrnfYfinrltgyLrn 166

RESULT 11

AAE11979

ID AAE11979 standard; Protein; 166 AA.  
XX AC AAE11979;  
XX DT 18-DEC-2001 (first entry)  
XX DE Human wild-type interferon (IFN) beta.  
XX KW Human; interferon-gamma; IFNG; interferon-beta; Interferon alpha; FSH;  
KW follicle stimulating hormone; granulocyte colony stimulating factor;  
KW G-CSF; Interleukin 10; IL-10; medicament; pulmonary administration;  
KW circulatory administration.  
XX OS Homo sapiens.  
XX PN WO200168141-A2.  
XX PD 20-SEP-2001.  
XX PF 16-MAR-2001; 2001WO-DK00182.  
XX PR 17-MAR-2000; 2000DK-0000447.  
XX PR 20-MAR-2000; 2000US-190844P.  
XX PR 25-AUG-2000; 2000WO-DK00471.  
XX PR 13-NOV-2000; 2000WO-DK00631.  
XX PA (MAXY-) MAXYGEN APS.  
XX PI Hansen CK;  
XX DR WPI; 2001-616274/71.  
XX PT Dispersions of particles for administration to the lung and circulatory  
PT system by inhalation, e.g. from a nebulizer -  
XX PS Claim 22; Page 136; 139pp; English.  
XX CC The present invention relates to novel dispersions of a conjugate  
CC comprising at least one non-polypeptide moiety covalently attached  
CC to a polypeptide variant, wherein the amino acid sequence of the  
CC polypeptide variant differs from that of the corresponding wild-type  
CC human polypeptide in that at least 1 residue comprising an attachment  
CC group for the non-polypeptide group has been introduced and/or removed.  
CC The wild-type human polypeptide is selected from the group consisting  
CC of interferon-gamma (IFNG), interferon-beta, interferon alpha, follicle  
CC stimulating hormone, (FSH), interleukin 10 (L-10) and granulocyte colony  
CC stimulating factor (G-CSF). The dispersion is used for the preparation  
CC of a medicament for pulmonary and/or circulatory administration. The  
CC present sequence is human wild type interferon (IFN) beta.  
XX SQ Sequence 166 AA;  
  
Query Match 98.6%; Score 863; DB 22; Length 166;  
Best Local Similarity 98.8%; Pred. No. 8.2e-70;  
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 MSYNLLGFLQSSNFQCKLLWQLNGRLEYCLKDRMNFDPPEIKQLQnFtKEDAALTIY 60  
Db 1 msynllgflqrssnfqckllwqlngrleyclkdrrmndfipeeikqlqfqkedaaltiy 60  
  
QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120  
Db 61 emlqnifalfrqdsstgwnetivenllanvyhqinhlktvleeklekedftrgklmssl 120  
  
QY 121 HLKRYYGRIILHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRLN 166  
Db 121 hlkryygrilhyllakeyshcawtivrveilrnfynrlitgylrn 166  
  
RESULT 12  
AAU00038  
ID AAU00038 standard; Protein; 166 AA.

XX AAU00038;  
XX DT 16-MAY-2001 (first entry)  
XX DE Human interferon beta.  
XX KW Human; interferon beta; antibody; multiple sclerosis; gene therapy;  
KW viral infection; viral hepatitis; cancer; breast cancer; inflammation;  
KW Crohn's disease; acute myeloid leukaemia; Hodgkin's disease;  
KW ulcerative colitis; immunomodulation.  
XX OS Homo sapiens.  
XX PN WO200115736-A2.  
XX PD 08-MAR-2001.  
XX PF 25-AUG-2000; 2000WO-DK00471.  
XX PR 27-AUG-1999; 99DK-0001197.  
XX PR 21-OCT-1999; 99US-0160782.  
XX PR 26-NOV-1999; 99DK-0001691.  
XX PR 07-FEB-2000; 2000DK-0000194.  
XX PR 07-MAR-2000; 2000DK-0000363.  
XX PR 14-APR-2000; 2000DK-0000642.  
XX PA (MAXY-) MAXYGEN APS.  
XX PI Pedersen AH, Schambye HT, Andersen KV, Bornaes C, Rasmussen PB;  
XX DR WPI; 2001-218488/22.  
XX DR N-PSDB; AAS00067.  
XX PT A conjugate exhibiting interferon beta activity useful for treating  
PT multiple sclerosis comprises a non-polypeptide group covalently  
PT attached to an interferon beta polypeptide -  
XX PS Example 1; Page 99-100; 108pp; English.  
XX CC The sequence is Human interferon beta. Conjugates of the invention  
CC exhibiting interferon beta activity comprise at least one first  
CC non-polypeptide group covalently attached to an interferon beta  
CC polypeptide, the amino acid sequence of which differs from wild-type  
CC human interferon beta in at least one introduced and at least one removed  
CC amino acid residue comprising an attachment group for the first  
CC non-polypeptide group. The invention also concerns reducing the  
CC immunogenicity and/or increasing functional in vivo half-life and/or  
CC serum half-life of an interferon beta polypeptide comprising introducing  
CC an amino acid residue constituting an attachment group for a first  
CC non-polypeptide group into a position exposed at the surface of the  
CC protein that does not contain such a group and removing an amino acid  
CC residue constituting an attachment group for a first non-polypeptide  
CC group and subjecting the modified peptide to conjugation with the  
CC non-polypeptide group. The conjugate and a cell culture expressing the  
CC mutated polypeptides are useful in the treatment of disease, especially  
CC multiple sclerosis, and for treating mammals having circulating  
CC antibodies against interferon beta 1a or 1b. DNA encoding the mutated  
CC proteins may be used for gene therapy. The DNA and proteins can also be  
CC used to treat viral infections (e.g viral hepatitis), cancer (e.g.  
CC breast cancer), inflammation, Crohn's disease, acute myeloid leukaemia,  
CC Hodgkin's disease and ulcerative colitis and for immunomodulation.  
XX SQ Sequence 166 AA;  
  
Query Match 98.6%; Score 863; DB 22; Length 166;  
Best Local Similarity 98.8%; Pred. No. 8.2e-70;  
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 MSYNLLGFLQSSNFQCKLLWQLNGRLEYCLKDRMNFDPPEIKQLQnFtKEDAALTIY 60  
Db 1 msynllgflqrssnfqckllwqlngrleyclkdrrmndfipeeikqlqfqkedaaltiy 60





CC and inflammatory diseases.

Sequence	1.66 AA;
SQ	

Query Match 98.6%; Score 863; DB 22; Length 166;

Best Local Similarity 98.8%; Pred. No. 8.2e-70;

Matches	164;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
---------	------	--------------	----	------------	----	--------	----	------	----

QY 1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQNFtKEDAALTY 60

\_\_\_\_\_

QY 61 EMLQNI FAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120

\_\_\_\_\_

Qy 121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLNR 166

\_\_\_\_\_

## RESULT 15

**AAB49357**

ID AAB49357 standard; Protein; 166 AA.

AC AAB49357;

AC AAB49357;

DT 07-MAR-20

DT 07-MAR-2001 (first entry)

DE Human INF-beta B-chain.

Interferon-beta activity; multiple sclerosis; cancer; viral infection;  
analogue.

XX

OS Homo sapiens.

PN WO200068387-A2.

PD 16-NOV-2000.

12-MAY-2000: 2000WO-US13216.

PR 12-MAY-1999: 99JIS-01333785

PA (XENC-) XENCOR INC

PT Bentzien, T.

XX  
DB WPT: 2001-007398/01

Novel interferon-beta activity (IbA) proteins which have greater stability than interferon-beta (IFN-beta) useful for the treatment of IFN-beta related disorders such as multiple sclerosis -

PS Example 1; Fig 1B; 109pp; English.

The present invention provides proteins which have interferon-beta (IFN-beta) activity. These analogues are produced so that they are less than 97% identical to human IFN-beta. They are useful in the treatment of multiple sclerosis, cancer, particularly osteosarcoma, basal cell carcinoma, cervical dysplasia, glioma, acute myeloid leukaemia, multiple myeloma, Hodgkin's disease, melanoma, and renal, liver and breast cancers, viral infections, including those caused by hepatitis viruses, herpes viruses and papilloma viruses, viral encephalitis, cytomegalovirus pneumonia and prophylaxis of rhinovirus, idiopathic pulmonary fibrosis and inflammatory diseases.

Sequence	166 AA;
SQ	

### Query Match

98.68: Score 863: DB 22: Length 166:

### Best Local Similarity

98.8%; Pred. No. 8.2e-70;

Matches	164;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
---------	------	--------------	----	------------	----	--------	----	------	----

QY 1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQnFtKEDAAALTIY 60

Db 1 msynllglqrssnfcqckllwqlngrlvcldkrmnfdipeekqlqrfkedaaltiy 60

QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDEFTRGKLMSSL 120

61 emlancifalgrdsstgwnetivellanyvghinhlktyleeklekedftrgklmssl 120

QY 121 HLKRYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRLN 166

```

11
Db
121 hlkryvqirilhyllkakeyshcawtlvrveellrnfyfnrltqyln 166

```

Search completed: July 29, 2002, 15:42:54

Job time: 230 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2002, 15:40:29 ; Search time 28.3 Seconds  
(without alignments)  
563.634 Million cell updates/sec

Title: SEQ2-49N-51S  
Perfect score: 874  
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGILRN 166  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	864	98.9	187	1 IVHUB1	interferon beta-1
2	482.5	55.2	186	1 IVBOB2	interferon beta-2
3	477.5	54.6	186	1 IVHOB1	interferon beta-1
4	451.5	51.7	186	1 IVBOB3	interferon beta-3
5	430.5	49.3	186	1 IVBOB1	interferon beta-1
6	336.5	38.5	182	1 IVMSB	interferon beta pr
7	328.5	37.6	184	2 JC5424	interferon beta pr
8	284	32.5	195	1 IVHO22	interferon alpha-I
9	263	30.1	195	1 IVHO21	interferon alpha-I
10	257	29.4	184	1 IVHOA2	interferon alpha-I
11	257	29.4	184	1 IVHOA3	interferon alpha-I
12	257	29.4	184	1 IVHOA1	interferon alpha-I
13	253	28.9	184	1 IVHOA2	interferon alpha-I
14	250.5	28.7	189	1 IVHU16	interferon alpha-I
15	250.5	28.7	189	2 I37584	IFN-alpha-N-protei
16	247.5	28.3	195	1 IVBOII	interferon alpha-I
17	245.5	28.1	165	2 I78570	alpha 2 interferon
18	245.5	28.1	172	2 A61578	trophoblast protei
19	245.5	28.1	195	2 A61455	trophoblast protei
20	244.5	28.0	188	1 IVHUA2	interferon alpha-2
21	244	27.9	195	1 IVHUII	interferon omega-1
22	243.5	27.9	189	1 IVHU4B	interferon alpha-I
23	241.5	27.6	167	2 F25843	interferon alpha-J
24	241.5	27.6	189	1 IVHUA7	interferon alpha-5
25	241.5	27.6	189	1 IVHUA0	interferon alpha-7
26	241.5	27.6	189	2 I53102	interferon-alpha-J
27	240.5	27.5	195	2 JS0204	trophoblast interf
28	239.5	27.4	189	2 I52347	interferon alpha-M
29	239.5	27.4	195	2 I47068	trophoblast protei

30	239.5	27.4	195	2 I47097	trophoblast protei
31	238.5	27.3	189	1 IVHUA9	interferon alpha-1
32	238	27.2	189	1 IVHUI4	interferon alpha-I
33	237.5	27.2	176	2 I56314	interferon-alpha -
34	237	27.1	195	2 A61403	interferon alpha-I
35	237	27.1	195	2 A53746	interferon, tropho
36	237	27.1	195	2 I46398	interferon, alpha -
37	237	27.1	195	2 S70011	interferon type I
38	237	27.1	195	2 I46974	interferon-omega45
39	236.5	27.1	189	2 I51970	interferon precurs
40	236.5	27.1	195	2 A39505	trophoblast interf
41	236.5	27.1	195	2 S23751	trophoblast interf
42	235.5	26.9	195	2 I47066	trophoblast protei
43	235	26.9	195	2 I46397	interferon alpha -
44	235	26.9	195	2 I46975	interferon-omega20
45	235	26.9	195	2 I46972	interferon-omega44

ALIGNMENTS

RESULT 1

IVHUB1  
interferon beta-1 precursor [validated] - human  
C;Species: Homo sapiens (man)  
C;Date: 18-Aug-1982 #sequence\_revision 18-Aug-1982 #text\_change 08-Dec-2000  
C;Accession: A93721; A93887; A91468; A93225; A93706; A93700; A93269; S04479; I56315;  
R;Lawn, R.M.; Adelman, J.; Franke, A.E.; Houck, C.M.; Gross, M.; Najarian, R.; Goedde  
Nucleic Acids Res. 9, 1045-1052, 1981  
A;Title: Human fibroblast interferon gene lacks introns.  
A;Reference number: A93721; MUID:81198952  
A;Accession: A93721  
A;Molecule type: DNA  
A;Residues: 1-187 <LAW>  
A;Cross-references: GB:V00535; NID:g32639; PIDN:CAA23796.1; PID:g32640  
R;Ohno, S.; Taniguchi, T.  
Proc. Natl. Acad. Sci. U.S.A. 78, 5305-5309, 1981  
A;Title: Structure of a chromosomal gene for human interferon beta.  
A;Reference number: A93887  
A;Accession: A93887  
A;Molecule type: DNA  
A;Residues: 1-187 <OHN>  
R;Taniguchi, T.; Ohno, S.; Fujii-Kuriyama, Y.; Muramatsu, M.  
Gene 10, 11-15, 1980  
A;Title: The nucleotide sequence of human fibroblast interferon cDNA.  
A;Reference number: A91468; MUID:81005095  
A;Accession: A91468  
A;Molecule type: mRNA  
A;Residues: 1-187 <TAN>  
A;Cross-references: GB:V00546; NID:g32735; PIDN:CAA23807.1; PID:g32736  
R;Derynck, R.; Content, J.; Declercq, E.; Volckaert, G.; Tavernier, J.; Devos, R.; Fi  
Nature 285, 542-547, 1980  
A;Title: Isolation and structure of a human fibroblast interferon gene.  
A;Reference number: A93225; MUID:80254542  
A;Accession: A93225  
A;Molecule type: DNA  
A;Residues: 1-187 <DER>  
A;Cross-references: GB:V00546; NID:g32735; PIDN:CAA23807.1; PID:g32736  
R;Houghton, M.; Eaton, M.A.W.; Stewart, A.G.; Smith, J.C.; Doel, S.M.; Cartlin, G.H.;  
Nucleic Acids Res. 8, 2885-2894, 1980  
A;Title: The complete amino acid sequence of human fibroblast interferon as deduced u  
A;Reference number: A93706; MUID:81053720  
A;Accession: A93706  
A;Molecule type: mRNA  
A;Residues: 1-187 <HOU>  
A;Cross-references: GB:J00218; GB:K00616; GB:M11029; NID:g184626; PID:g386802  
R;Houghton, M.; Stewart, A.G.; Doel, S.M.; Emtage, J.S.; Eaton, M.A.W.; Smith, J.C.;  
Nucleic Acids Res. 8, 1913-1931, 1980  
A;Title: The amino-terminal sequence of human fibroblast interferon as deduced from r  
A;Reference number: A93700; MUID:81053854  
A;Accession: A93700  
A;Molecule type: mRNA  
A;Residues: 1-68 <HO2>





A;Accession: A01841  
A;Molecule type: DNA  
A;Residues: 1-186 <LEU>  
C;Superfamily: interferon alpha  
C;Keywords: glycoprotein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-186/Product: interferon beta-3 #status predicted <MAT>  
F;52-161/Disulfide bonds: #status predicted  
F;131,173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.7%; Score 451.5; DB 1; Length 186;  
Best Local Similarity 52.7%; Pred. No. 1.1e-29;  
Matches 87; Conservative 34; Mismatches 43; Indels 1; Gaps 1;

QY 2 SYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDPPEEIKQLQnFsKEDAALTIYE 61  
||:|| | | | | ||||| ||: :||: :||: ||: | | | |||| | |||  
Db 23 SYSLLRFQQRSAEVCQKLLGQLHSTPQHCLAKMDFQVPEEMNQAOQFRKEDAILVIYE 82

QY 62 MLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLH 121  
||| || | : | ||||:||||:|| : | | | : : : : || | : ||  
Db 83 MLQQIFNILTRDFSSTGWSETIIEDLLVELYGQMRNLQPIQKEIMQEQNFTMGD-TTVLH 141

QY 122 LKRYYGRILHYLKAKEYSHCAWTIVRVEILRNPYFINRLTGYLRN 166  
||:|| : : ||:||||: ||||:||||: || | | | : ||| ||:  
Db 142 LKKYYFNLVQYLESKEYNRCAWTVVRVQILTNFSLMRLTASLRD 186

RESULT 5  
IVBOB1  
interferon beta-1 precursor - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 15-Nov-1984 #sequence\_revision 15-Nov-1984 #text\_change 07-Feb-1997  
C;Accession: A01842  
R;Leung, D.W.; Capon, D.J.; Goeddel, D.V.  
Bio/Technology 2, 458-464, 1984  
A;Title: The structure and bacterial expression of three distinct bovine interferon-beta  
A;Reference number: A90097  
A;Accession: A01842  
A;Molecule type: DNA  
A;Residues: 1-186 <LEU>  
C;Superfamily: interferon alpha  
C;Keywords: glycoprotein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-186/Product: interferon beta-1 #status predicted <MAT>  
F;52-161/Disulfide bonds: #status predicted  
F;131,173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 49.3%; Score 430.5; DB 1; Length 186;  
Best Local Similarity 50.3%; Pred. No. 5.7e-28;  
Matches 83; Conservative 36; Mismatches 45; Indels 1; Gaps 1;

QY 2 SYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDPPEEIKQLQnFsKEDAALTIYE 61  
||:|| | | | | :|||| | :||: ||: ||: ||: ||: ||: || | |||| | :||  
Db 23 SYSLLRFQQRSLKECQKLLGQLPSTSQHCLEARMDFQMPEEMKQEQQFKEDAILVMYE 82

QY 62 MLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLH 121  
:||:| | : | ||||:||||:|| : | | | : : | : ||: | : |  
Db 83 VLQHIFGILTRDFSSTGWSETIIEDLLKELYQMNRNLQPIQKEIMQKONSTTDTIVP-H 141

QY 122 LKRYYGRILHYLKAKEYSHCAWTIVRVEILRNPYFINRLTGYLRN 166  
| : || : : ||:|||| ||||:|||| | : | ||||:|:  
Db 142 LGKYYFNLVQYLESKEYDRCAWTVVQVQILTNVSLMRLTGYVRD 186

RESULT 6  
IVMSB  
interferon beta precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #text\_change 22-Jun-1999  
C;Accession: S02020; S04201; A01839  
R;Vodjdani, G.; Coulombel, C.; Doly, J.

J. Mol. Biol. 204, 221-231, 1988  
A;Title: Structure and characterization of a murine chromosomal fragment containing t  
A;Reference number: S02020; MUID:89125582  
A;Accession: S02020  
A;Molecule type: DNA  
A;Residues: 1-182 <VOD>  
A;Cross-references: EMBL:X14029; NID:g51550; PIDN:CAA32190.1; PID:g51551  
R;Kuga, T.; Fujita, T.; Taniguchi, T.  
Nucleic Acids Res. 17, 3291, 1989  
A;Title: Nucleotide sequence of the mouse interferon-beta gene.  
A;Reference number: S04201; MUID:89263735  
A;Accession: S04201  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-182 <KUG>  
A;Cross-references: EMBL:X14455; NID:g51538; PIDN:CAA32625.1; PID:g51539  
R;Higashi, Y.; Sokawa, Y.; Watanabe, Y.; Kawade, Y.; Ohno, S.; Takaoka, C.; Taniguchi  
J. Biol. Chem. 258, 9522-9529, 1983  
A;Title: Structure and expression of a cloned cDNA for mouse interferon-beta.  
A;Reference number: A01839; MUID:83265757  
A;Accession: A01839  
A;Molecule type: mRNA  
A;Residues: 1-182 <HIG>  
A;Cross-references: GB:K00020; NID:g194113; PIDN:AAA37891.1; PID:g309327  
C;Genetics:  
A;Map position: 4  
C;Superfamily: interferon alpha  
C;Keywords: glycoprotein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-182/Product: interferon beta #status predicted <MAT>  
F;50,90,97/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 38.5%; Score 336.5; DB 1; Length 182;  
Best Local Similarity 45.8%; Pred. No. 2.4e-20;  
Matches 76; Conservative 26; Mismatches 59; Indels 5; Gaps 3;

QY 1 MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDPPEEIKQLQnFsKEDAALTIY 60  
:| | | : ||: || ||||: | | : | | | : | | |  
Db 22 INYKQLQQLQERTNIRKQCQELLEQLNGKIN--LTYRADFKIPMEM--TEKMQKSYTAFAIQ 77

QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120  
||||:| : || : ||||| || | : | | ||||| : | | : |  
Db 78 EMLQNVFLVFRNFSSTGWNETIVVRLDELHQQTVFLKTVLEEK-QEERLTWEMSSTAL 136

QY 121 HLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNPYFINRLTGYLRN 166  
||| || | : || : | : || || || || || || : |  
Db 137 HLKSYVWRVQRYLKLKMKNSYAMVVRAEIFRNLRIIRLRTNRFQN 182

RESULT 7  
JC5424  
interferon beta precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 10-Jun-1997 #sequence\_revision 18-Jul-1997 #text\_change 20-Jun-2000  
C;Accession: JC5424  
R;Yokoyama, S.; Ohishi, N.; Shamoto, M.; Watanabe, Y.; Yagi, K.  
Biochem. Biophys. Res. Commun. 232, 698-701, 1997  
A;Title: Isolation and expression of rat interferon beta gene and growth-inhibitory e  
A;Reference number: JC5424; MUID:97271387  
A;Accession: JC5424  
A;Molecule type: DNA  
A;Residues: 1-184 <YOK>  
A;Cross-references: DDBJ:D87919; NID:g1616938; PIDN:BAA13502.1; PID:g1616939  
C;Comment: This protein exhibits characteristic antiviral and antitumor activities.  
C;Genetics:  
A;Gene: IFNbeta  
C;Superfamily: interferon alpha  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-184/Product: interferon beta #status predicted <MAT>

Query Match 37.6%; Score 328.5; DB 2; Length 184;

```

Best Local Similarity 45.2%; Pred. No. 1.le-19;
Matches 75; Conservative 23; Mismatches 65; Indels 3; Gaps 2;

QY 1 MSYNLLGFLQRSSNFQCQLLWQLNGRLEYCLKDRMNFDPPEEIKQLQnFsKEDAALTIY 60
   : | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 22 IDYKQLQFRQSTSIRTCCKLLRQLNGLRN--LSYRTDFKIPMEVVMHPMSOMEKSYSATAFIQ 79

QY 61 EMLQNIFAIFRODSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSL 120
   |||||:|:||:|||||:|||||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 80 VMLQNVFLVFRSFSSTGWNETIVESLLDELHQQTELEILLKEK-QEERLTWTVTSTTL 138

QY 121 HLKRYVGRILHYLKAKKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 166
   || || |: ||| |:|: || |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 139 GLKSYWRVRQYLKDKKYNSYAMVVRAEVRNFSIILRLNRNQFN 184

RESULT 8
IVHO22
interferon alpha-II-2 precursor - horse
N:Alternate names: EqIFN-alpha-II-2; EqIFN-omega-2; type I interferon
C:Species: Equus caballus (domestic horse)
C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 22-Jun-1999
C:Accession: F24912
R:Himmeler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.
DNA 5, 345-356, 1986
A:Title: Molecular cloning and expression in Escherichia coli of equine type I
A:Reference number: A90956; MUID:87053170
A:Accession: F24912
A:Molecule type: DNA
A:Residues: 1-195 <HIM>
A:Cross-references: GB:M14545; NID:g164217; PIDN:AAA30949.1; PID:g164220
C:Superfamily: interferon alpha
C:Keywords: antiviral; glycoprotein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-195/Product: interferon alpha-II-2 #status predicted <MAT>
F:24-122,52-162/Disulfide bonds: #status predicted
F:101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 32.5%; Score 284; DB 1; Length 195;
Best Local Similarity 36.6%; Pred. No. 4.7e-16;
Matches 60; Conservative 33; Mismatches 57; Indels 14; Gaps 1;

QY 2 SYNLLGFLQRSSNFQCQLLWQLNGRLEYCLKDRMNFDPPEEIKQLQnFsKEDAALTIYE 61
   ::|||::|:|: |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 37 NFVLLGQMSRISS-----AICLKDRKDFRPQDMADGRQFPEAQAAASVLHE 82

QY 62 MLQNIFAIFRODSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSLH 121
   ||| |||::|:| |||::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 83 MLQQIFSLSFHTERSAAWNNTLLDELCTGLLRQLEDLDTCLEQEMGEESALGTVPFLA 142

QY 122 LKRYVGRILHYLKAKKEYSHCAWTIVRVEILRNFFYNRLTGYLR 165
   :|||:| ||| |:| ||| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 143 VKRYFRGIHLYLKKEYSDCAWEIVRMEIMRSFSSSANLQGRLR 186

RESULT 9
IVHO21
interferon alpha-II-1 precursor - horse
N:Alternate names: EqIFN-alpha-II-1; EqIFN-omega-1; type I interferon
C:Species: Equus caballus (domestic horse)
C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 22-Jun-1999
C:Accession: E24912
R:Himmeler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.
DNA 5, 345-356, 1986
A:Title: Molecular cloning and expression in Escherichia coli of equine type I
A:Reference number: A90956; MUID:87053170
A:Accession: E24912
A:Molecule type: DNA
A:Residues: 1-195 <HIM>
A:Cross-references: GB:M14544; NID:g164230; PIDN:AAA30955.1; PID:g164231
C:Superfamily: interferon alpha
C:Keywords: antiviral; glycoprotein

```

```

F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-195/Product: interferon alpha-II-1 #status predicted <MAT>
F;24-122,52-162/Disulfide bonds: #status predicted
F;101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          30.1%; Score 263; DB 1; Length 195;
Best Local Similarity 40.3%; Pred. No. 2.4e-14;
Matches 54; Conservative 26; Mismatches 54; Indels 0; Gaps 0;

QY 31 CLKDRMNFDIPEEIKQLQNFsKEDAAALTIYEMLQNFPAIFRQDSSSTGWNETIVENLLAN 90
Db 52 CLKHRTDFRPEQELDGRQPEAQATSVLQEMLQQIVSLFHTERSAAWNTTLLDRLLAG 111

QY 91 VYHQINHLKTVLEEKLEKEDFTRGKLMSSHLKRYVGRILHYLKAKEYSHCAWTIVRVEI 150
Db 112 LHQOLEDLNTCLDEQTGEESALGTGPTLAVKRYFRIRLYLTEKKYSDCAWEIVRVDI 171

QY 151 LRNFYFINRLTGYL 164
Db 172 MRSFSSSANLQRL 185

RESULT 10
IVHOA4
interferon alpha-I-4 precursor - horse
N:Alternate names: EqIFN-alpha-I-4; type I interferon
C:Species: Equus caballus (domestic horse)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Jun-1999
C:Accession: D24912
R:Himmlier, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.
DNA 5, 345-356, 1986
A:Title: Molecular cloning and expression in Escherichia coli of equine type I interf
A:Reference number: A90956; MUID:87053170
A:Accession: D24912
A:Molecule type: DNA
A:Residues: 1-184 <HIM>
A:Cross-references: GB:M14543; NID:g164224; PIDN:AAA30952.1; PID:g164225
C:Superfamily: interferon alpha
C:Keywords: antiviral
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-184/Product: interferon alpha-I-4 #status predicted <MAT>
F;24-122,52-162/Disulfide bonds: #status predicted

Query Match          29.4%; Score 257; DB 1; Length 184;
Best Local Similarity 36.0%; Pred. No. 6.7e-14;
Matches 54; Conservative 28; Mismatches 54; Indels 14; Gaps 1;

QY 5 LLGFLQRSSNFQCQLLWQLNGRLEYCLKDRMNFDPPEEIKQLQNFsKEDAAALTIYEMLQ 64
Db 40 LLGQMRRI SPFS-----CLKDRNDFGFPQEVFDGNQFRKPKQAI SAHVETIQ 85

QY 65 NIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSHLKLR 124
Db 86 QIFHLFSTDGSSAAWDESLDKLYTGLYQQLTELEACL SQEVGVEETPLMNEDSLLAVRR 145

QY 125 YVGRILHYLKAKEYSHCAWTIVRVEILRN 154
Db 146 YFQRITLYLQEKKYSPCAWEIVRAEIMRSF 175

RESULT 11
IVHOA3
interferon alpha-I-3 precursor - horse
N:Alternate names: EqIFN-alpha-I-3; type I interferon
C:Species: Equus caballus (domestic horse)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Jun-1999
C:Accession: C24912
R:Himmlier, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.
DNA 5, 345-356, 1986
A:Title: Molecular cloning and expression in Escherichia coli of equine type I interf
A:Reference number: A90956; MUID:87053170

```

A:Accession: C24912  
A:Molecule type: DNA  
A:Residues: 1-184 <HIM>  
A:Cross-references: GB:M14542; NID:g164222; PIDN:AAA30951.1; PID:g1642223  
C:Superfamily: interferon alpha  
C:Keywords: antiviral  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-184/Product: interferon alpha-I-3 #status predicted <MAT>  
F:24-122,52-162/Dissulfide bonds: #status predicted

Query Match	29.4%;	Score 257;	DB 1;	Length 184;
Best Local Similarity	36.0%;	Pred. No. 6.7e-14;		
Matches 54;	Conservative 28;	Mismatches 54;	Indels 14;	Gaps 1;

QY 5 LLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFEDIPEEIKQLQNFsKEDAAALTIYEMLQ 64  
 |||::||| | ||||:| ||||:| |||:| |||:| |||:|  
 Db 40 LLGQMRRISPFs-----CLKDRNDFGFPPQEVFDGNGQFRKPQAIASAVHETIQ 85  
 QY 65 NIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDETRGKLMSSSLHLKR 124  
 ||:| ||| |||:::| |:|:| |:|:| |:|:| |:|:| |:|:|  
 Db 86 QIFHLFSTDGSSAAWDESLDLKLYGLYQQLTELEACLSEQVGVVEPTLMNEDSLLAVRR 145  
 QY 125 YYGRILHYLKAKEYSHCAWTIVRVEILRNF 154  
 |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|  
 Db 146 YFORIALYLOEKKYSPCAWEIVRAEIMRSF 175

RESULT 12  
IVHOA1  
interferon alpha-I-1 precursor - horse  
N;Alternate names: EqIFN-alpha-I-1; type I interferon  
C;Species: Equus caballus (domestic horse)  
C;Date: 28-Dec-1987 #sequence\_revislon 28-Dec-1987 #text\_change 18-Jun-1999  
C;Accession: A24912

R;Himmeler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.  
DNA 5, 345-356, 1986  
A;Title: Molecular cloning and expression in Escherichia coli of equine type I interferon  
A;Reference number: A90956; MUID:87053170  
A;Accession: A24912  
A;Molecule type: DNA  
A;Residues: 1-184 <HIM>  
A;Cross-references: GB:M14540; NID:gl64226; PIDN:AAA30953.1; PID:gl64227  
C;Superfamily: Interferon alpha  
C;Keywords: antiviral  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-184/Product: interferon alpha-I-1 #status predicted <MAT>  
F;24-122,52-162/Disulfide bonds: #status predicted

Query Match 29.4%; Score 257; DB 1; Length 184;  
Best Local Similarity 36.0%; Pred. No. 6.7e-14;  
Matches 54; Conservative 28; Mismatches 54; Indels 14; Gaps 1;

```

QY      5 LLGLFLQRSSNFQCCKLLWQLNGRLEYCLKDRMNFEDIPEETIKQLQNfSKEDAAALTIYEMLQ   64
       |||::||| |         |||||::|||::| | | |::|:|
Db     40 LLGQMRRISPFs-----CLKDRNDFGFQPQEVFDGNQFRKPQAISAVHETIQ   85
QY     65 NIFAIFRDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDETRGKLMSSLHLKR   124
       |||::||| |::|::| |::|:| |::|:|:| |::|:|
Db     86 QIFHLFSTDGSSAANDESLLDKLYTGLYQQLTELEACLSEQVGVEEPTLMNEDSLLAVRR   145
QY    125 YYGRILHYLKAKKEYSHCAWTIVRVVEILRNf   154
       |:| |::|:|:| |::| |::| |::|:|
Db    146 YFORIALYLQEKKYSPCaweIvRAeiMRsf   175

```

```

RESULT# 13
IVHOA2
N:Interferon alpha-I-2 precursor - horse
N:Alternate names: EqIFN-alpha-I-2; type I interferon
C:Species: Equus caballus (domestic horse)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Jun-1999

```

C;Accession: B24912  
R;Himmeler, A.; Hauptmann, R.; Adolf, G.R.; Swetly, P.  
DNA 5, 345-356, 1986  
A;Title: Molecular cloning and expression in Escherichia coli of equine  
A;Reference number: A90956; MUID:87053170  
A;Accession: B24912  
A;Molecule type: DNA  
A;Residues: 1-184 <HIM>  
A;Cross-references: GB:M14541; NID:gl64218; PIDN:AAA30950.1; PID:gl64221  
C;Superfamily: interferon alpha  
C;Keywords: antiviral  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-184/Product: interferon alpha-I-2 #status predicted <MAT>  
F;24-122,52-162/Disulfide bonds: #status predicted

Query Match 28.9%; Score 253; DB 1; Length 184;  
Best Local Similarity 36.0%; Pred. No. 1.4e-13;  
Matches 54; Conservative 27; Mismatches 55; Indels 14; Gaps 1;

```
Qy      5 LLGFLQRSSNFQCCKLLWQLNGRLEYCLKDRMFDIPEEIKQLQNfSKEDAALTIYEMLQ 64  
         |||::|||   |||||::|||::|||::|||::|||:  
Db     40 LLQMRRISPFs-----CLKRDNDFGFQPQEVFDGNFQRKPQAISAHVETIQ 85  
  
Qy     65 NIFAIFRODSSSTGWNETIVENLLANVYHQINHLKTIVLEEKLEKEDEFTACKLMSSLHLKR 12  
         ||:|||:||||:|::|||::|::|||::|::|||:  
Db     86 QIFHLFSTDGSSAAWDESLLDKLYTGLYQQLTELEACLSEQEVGVETPLMNEDSLLAVRR 14  
  
Qy    125 YYGRILHYLKAEKEYSHCAWTIVRVIELRNF 154  
       -:|||:|::|::|::|::|::|::|::|:  
Db   146 YFORIALYLOEKKYSPCAWAIVRAEIMRCF 175
```

```

RESULT 14
IVHU16
interferon alpha-I-16 precursor - human
N;Alternate names: HuIFN-alpha-I-16; interferon alpha-I-WA; type I interferon
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Jun-1999
C;Accession: G23753; A22068; I73334
R;Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.;
J. Mol. Biol. 185, 227-260, 1985
A;Title: Structural relationship of human interferon alpha genes and pseudogenes.
A;Reference number: A92916; MUID:86037205

```

C:Genetics.  
A:Gene: GDB:IFNA16  
A:Cross-references: GDB:136357; OMIM:147580  
A:Map position: 9p22-9p22  
A:Introns: #status absent  
C:Superfamily: interferon alpha  
C:Keywords: antiviral; cytokine; leukocyte  
F:1-23/Domain: signal sequence #status predicted





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 29, 2002, 15:44:50 ; Search time 46.62 Seconds  
(without alignments)  
615.984 Million cell updates/sec

Title: SEQ2-49N-51T  
Perfect score: 875  
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRLN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	821	93.8	187	6	077812 macaca fasc
2	816	93.3	187	4	Q15943 homo sapien
3	524.5	59.9	186	6	Q29412 sus scrofa
4	254.5	29.1	195	6	Q9GLL5 bos taurus
5	249.5	28.5	189	4	Q14618 homo sapien
6	244.5	27.9	188	4	Q96KI6 homo sapien
7	244	27.9	195	6	Q28844 oryctolagus
8	243	27.8	189	6	Q95J78 saguinus oe
9	241	27.5	189	6	Q95J77 homo sapien
10	240.5	27.5	189	4	Q14607 bos taurus
11	238.5	27.3	195	6	Q9GLL6
12	236	27.0	174	4	Q13168 homo sapien
13	236	27.0	195	6	Q28845 oryctolagus
14	236	27.0	195	6	Q28562 ovis aries
15	236	27.0	195	6	Q28545 ovis aries
16	235.5	26.9	189	4	Q14639 homo sapien

17	235.5	26.9	195	6	Q9MYK6	Q9myk6 bos taurus
18	235.5	26.9	195	6	Q95NE2	Q95ne2 bos taurus
19	234	26.7	195	6	Q28843	Q28843 oryctolagus
20	234	26.7	195	6	Q28847	Q28847 oryctolagus
21	234	26.7	195	6	Q28561	Q28561 ovis aries
22	225	25.7	190	6	Q29085	Q29085 sus scrofa
23	224.5	25.7	179	6	Q29084	Q29084 sus scrofa
24	222.5	25.4	195	6	P28170	P28170 ovis aries
25	220.5	25.2	181	4	Q14608	Q14608 homo sapien
26	219	25.0	190	6	Q29098	Q29098 sus scrofa
27	217	24.9	190	11	Q9ES91	Q9es91 marmota mon
28	217	24.8	166	4	Q9UMJ3	Q9umj3 homo sapien
29	217	24.8	189	4	Q14605	Q14605 homo sapien
30	215.5	24.6	207	4	Q9P0W0	Q9p0w0 homo sapien
31	212	24.2	190	11	Q61719	Q61719 mus musculu
32	208	23.8	190	11	Q99N22	Q99n22 marmota mon
33	200	22.9	190	11	Q64138	Q64138 cricetinae
34	197	22.5	84	6	Q95LB8	Q95lb8 sus scrofa
35	195.5	22.3	170	6	Q29114	Q29114 sus scrofa
36	193.5	22.1	170	6	Q29115	Q29115 sus scrofa
37	193	22.1	190	11	Q61718	Q61718 mus musculu
38	193	22.1	190	11	Q91WX3	Q91wx3 sigmodon hi
39	188	21.5	108	6	Q9N1U6	Q9nlu6 equus cabal
40	186	21.3	166	6	P79228	P79228 odocoileus
41	185	21.1	190	11	Q61716	Q61716 mus musculu
42	180	20.6	136	11	Q61717	Q61717 mus musculu
43	150.5	17.2	182	11	Q9RLT0	Q9rlt0 mus musculu
44	147.5	16.9	193	13	Q9PW15	Q9pwi5 gallus gall
45	132.5	15.1	193	13	Q9PW16	Q9pwi6 gallus gall

ALIGNMENTS

RESULT	1
O77812	O77812
ID	O77812
AC	O77812;
DT	01-NOV-1998 (TremBLrel. 08, Created)
DT	01-NOV-1998 (TremBLrel. 08, Last sequence update)
DT	01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE	INTERFERON BETA.
GN	IFN-BETA.
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC	Cercopitheidae; Macaca.
OX	NCBI_TaxID=9541;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=99156140; PubMed=10048395;
RA	Matheux F., Le Grand R., Rousseau V., De Maeyer E., Dormont D.,
RA	Lauret E.;
RT	"Macaque lymphocytes transduced by a constitutively expressed
RT	interferon beta gene display an enhanced resistance to SIVmac251
RT	infection.";
RL	Hum. Gene Ther. 10:429-429(1999).
CC	-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC	FAMILY.
DR	EMBL; AJ011909; CAA09862.1; -.
DR	HSSP; P01574; 1AU1.
DR	InterPro; IPR000471; Interferon_abd.
DR	Pfam; PF00143; interferon; 1.
DR	PRINTS; PR00266; INTERFERONAB.
DR	ProDom; PD000550; Interferon_abd; 1.
DR	SMART; SM00076; IFabd; 1.
DR	PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW	Antiviral; Cytokine.
SQ	SEQUENCE 187 AA; 22266 MW; 376AEF73332B7807 CRC64;
Query Match 93.8%; Score 821; DB 6; Length 187;	
Best Local Similarity 92.8%; Pred. No. 1e-63;	





```
DR HSSP; P01563; 2HIE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine.
SQ SEQUENCE 195 AA; 21981 MW; D4D2E3EF5134AE5F CRC64;

Query Match      27.9%; Score 244; DB 6; Length 195;
Best Local Similarity 41.1%; Pred. No. 1.1e-13;
Matches 51; Conservative 20; Mismatches 53; Indels 0; Gaps 0;

QY 31 CLKDRMNFDIPEEIKQLQnFTKEDAALTIYEMLQNIFAIFRQDSSSTGWNETIVENLLAN 90
   ||||| :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 52 CLKDRRDFQFPREVVNGSQFKHQAVSVLHEMLQQIFNLLHTAHSSAAWNTLLEELHAA 111

QY 91 VYHQINHLKTVLEEKLEKEDFTRGKLMSSLHLKRYGRILHYLKAKEYSHCAWTIVRVEI 150
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 112 LHQQLQGLTCLVQAMGEEDSVLTADPTMLKRYFQRIRLYLDEKKHSGCAWELVRMEI 171

QY 151 LRNF 154
   | |
Db 172 RRAF 175

RESULT 8
Q95J78
ID Q95J78 PRELIMINARY; PRT; 189 AA.
AC Q95J78;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERFERON-ALPHA PRECURSOR.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 189 POTENTIAL.
SQ SEQUENCE 189 AA; 21937 MW; 06A45DD2B631C85C CRC64;

Query Match      27.8%; Score 243; DB 6; Length 189;
Best Local Similarity 33.3%; Pred. No. 1.3e-13;
Matches 54; Conservative 29; Mismatches 65; Indels 14; Gaps 1;

QY 5 LLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQnFTKEDAALTIYEMLQ 64
   || :|| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 40 LLAQMRRISFPS-----CLKDRRDFEFPQEEFDGNQFKARAIFVLHEMIQ 85

QY 65 NIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLHLKR 124
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 86 QTFNLFSTKDSSAAWDETLLDKFRTELYQQLEACVQVQEVGVTDTPLLNEDSILTVRK 145

QY 125 YYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN 166
   | :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 146 YFQRITLYLKEKKYSACAWEVVRAEIMRSFSLSTNLQKGLRS 187

RESULT 9
Q95J77
```

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ID Q95J77 PRELIMINARY; PRT; 189 AA.
AC Q95J77;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERFERON-ALPHA PRECURSOR.
GN IFN-ALPHA.
OS Saguinus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RA Ceccacci A., Aurisicchio L., Ciliberto G., Palombo F., Traboni C.;
RT "Recombinant cotton-top tamarin interferon: a new tool for a primate
   hepatitis model.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250196; CAC44125.1; -.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 189 INTERFERON-ALPHA.
SQ SEQUENCE 189 AA; 22052 MW; 9E4389CFEC329DBA CRC64;

Query Match      27.5%; Score 241; DB 6; Length 189;
Best Local Similarity 36.0%; Pred. No. 1.9e-13;
Matches 49; Conservative 27; Mismatches 60; Indels 0; Gaps 0;

QY 31 CLKDRMNFDIPEEIKQLQnFTKEDAALTIYEMLQNIFAIFRQDSSSTGWNETIVENLLAN 90
   ||||| :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 52 CLKDRRDFEFPQEEFDNQQFKARAIFVLHEMIQQTFFNLFSTKDSSAAWDETLLDKFRTE 111

QY 91 VYHQINHLKTVLEEKLEKEDFTRGKLMSSLHLKRYGRILHYLKAKEYSHCAWTIVRVEI 150
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 112 LYQQLNELEACVMQEVGVTDTPLLNEDSILTVRKYFQRIITLYLKEKKYSACAWEVVRAEI 171

QY 151 LRNFYFINRLTGYLRN 166
   :| | | | | | | |
Db 172 MRSFSLSTNLQKGLRS 187

RESULT 10
Q14607
ID Q14607 PRELIMINARY; PRT; 189 AA.
AC Q14607;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE INTERFERON-ALPHA-J1 (IFN-ALPHA-J1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86005847; PubMed=2995168;
RA Cohen S., Velan B., Grosfeld H., Shalita Z., Leitner M.,
   Shaffer A.;
RT "Cloning, expression and biological activity of a new variant of human
   interferon alpha identified in virus induced lymphoblastoid cells.";
RL Dev. Biol. 60:111-122(1985).
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
   FAMILY.
CC EMBL; M34913; AAA36039.1; -.
DR HSSP; P01563; 2HIE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine.
SQ SEQUENCE 189 AA; 22048 MW; 2AF6F48447BB72B3 CRC64;
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DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine.
SQ SEQUENCE 195 AA; 21996 MW; 395EE700C586A928 CRC64;

Query Match      27.0%; Score 236; DB 6; Length 195;
Best Local Similarity 39.5%; Pred. No. 5.3e-13;
Matches 49; Conservative 20; Mismatches 55; Indels 0; Gaps 0;

QY 31 CLKDRMNFDIPEEIKQLQnFtKEDAAItIYEMlQNlFAlFRQDSSStGWNtIVENllAN 90
    ||||| : | | | : | | | : ||||| : | | | : ||||| : | | | : ||||| :
Db 52 CLKDRRDFQFPREVNGSQFQKNQTVSVLHEMLQQlFNLlHTARSSAAWNtLLEELHTA 111

QY 91 VYHQINHLKtVLEEKLEKEDfTRGKLmSSlHLKRYyGRlLHYLKAKEYSHCAWtIVRVEI 150
    :: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 112 LHQQLQGLetCLVQAMGEEDSVLTADsPTlMLKRYfQRIrLYLDEKKHSGCAWELVRMEI 171

QY 151 LRNF 154
    | |
Db 172 RRAF 175

RESULT 14
Q28562
ID Q28562 PRELIMINARY; PRT; 195 AA.
AC Q28562;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE OVINE INTERFERON ALPHA PRECURSOR.
GN AMY 49.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92039090; PubMed=1937057;
RA Whaley A.E., Carroll R.S., Imakawa K.;
RT "Cloning and analysis of a gene encoding ovine interferon alpha-II.";
RL Gene 106:281-282(1991).
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
    FAMILY.
DR EMBL; X59068; CAA41791.1; -.
DR HSSP; P01563; 2HIE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 195 OVINE INTERFERON ALPHA.
SQ SEQUENCE 195 AA; 22006 MW; 3B8EE700C586A928 CRC64;

Query Match      27.0%; Score 236; DB 6; Length 195;
Best Local Similarity 39.5%; Pred. No. 5.3e-13;
Matches 49; Conservative 20; Mismatches 55; Indels 0; Gaps 0;

QY 31 CLKDRMNFDIPEEIKQLQnFtKEDAAItIYEMlQNlFAlFRQDSSStGWNtIVENllAN 90
    ||||| : | | | : | | | : ||||| : | | | : ||||| : | | | : ||||| :
Db 52 CLKDRRDFQFPREVNGSQFQKNQTVSVLHEMLQQlFNLlHTARSSAAWNtLLEELHTA 111

QY 91 VYHQINHLKtVLEEKLEKEDfTRGKLmSSlHLKRYyGRlLHYLKAKEYSHCAWtIVRVEI 150
    :: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 52 CLKDRRDFQFPREVNGSQFQKNQTVSVLHEMLQQlFNLlHTARSSAAWNtLLEELHTA 111

QY 91 VYHQINHLKtVLEEKLEKEDfTRGKLmSSlHLKRYyGRlLHYLKAKEYSHCAWtIVRVEI 150
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Db 112 LHQQLQGLetCLVQAMGEEDSVLTADsPTlMLKRYfQRIrLYLDEKKHSGCAWELVRMEI 171
QY 151 LRNF 154
    | |
Db 172 RRAF 175

RESULT 15
Q28545
ID Q28545 PRELIMINARY; PRT; 195 AA.
AC Q28545;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INTERFERON TYPE I PRECURSOR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96219886; PubMed=8639714;
RA Liu L., Leaman D.W., Bixby J.A., Roberts R.M.;
RT "A type I ovine interferon with limited similarity to IFN-alpha, IFN-
RT omega and IFN-tau: gene structure, biological properties and unusual
RT species specificity.";
RL Biochim. Biophys. Acta, Gene Struct. Expr. 1294:55-62(1996).
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
    FAMILY.
DR EMBL; U26254; AAB06828.1; -.
DR HSSP; P01563; 2HIE.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; Interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Antiviral; Cytokine; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 195 INTERFERON TYPE I.
SQ SEQUENCE 195 AA; 22010 MW; 15C4CD45D582F86E CRC64;

Query Match      27.0%; Score 236; DB 6; Length 195;
Best Local Similarity 39.5%; Pred. No. 5.3e-13;
Matches 49; Conservative 20; Mismatches 55; Indels 0; Gaps 0;

QY 31 CLKDRMNFDIPEEIKQLQnFtKEDAAItIYEMlQNlFAlFRQDSSStGWNtIVENllAN 90
    ||||| : | | | : | | | : ||||| : | | | : ||||| : | | | : ||||| :
Db 52 CLKDRRDFQFPREVNGSQFQKNQTVSVLHEMLQQlFNLlHTARSSAAWNtLLEELHTA 111

QY 91 VYHQINHLKtVLEEKLEKEDfTRGKLmSSlHLKRYyGRlLHYLKAKEYSHCAWtIVRVEI 150
    :: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 112 LHQQLQGLetCLVQAMGEEDSVLTADsPTlMLKRYfQRIrLYLDEKKHSGCAWELVRMEI 171

QY 151 LRNF 154
    | |
Db 172 RRAF 175

Search completed: July 29, 2002, 15:44:50
Job time: 196 sec
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 29, 2002, 15:42:04 ; Search time 15.89 Seconds  
(without alignments)  
404.496 Million cell updates/sec

Title: SEQ2-49N-51S  
Perfect score: 874  
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	864	98.9	187	1 INB_HUMAN	P01574 homo sapien
2	516.5	59.1	186	1 INB_FELCA	Q9n2j0 felis silve
3	482.5	55.2	186	1 INB2_BOVIN	P01576 bos taurus
4	477.5	54.6	186	1 INB_HORSE	P05012 equus cabal
5	451.5	51.7	186	1 INB3_BOVIN	P01577 bos taurus
6	430.5	49.3	186	1 INB1_BOVIN	P01578 bos taurus
7	336.5	38.5	182	1 INB_MOUSE	P01575 mus musculu
8	328.5	37.6	184	1 INB_RAT	P70499 rattus norv
9	284	32.5	195	1 INO2_HORSE	P05002 equus cabal
10	263	30.1	195	1 INO1_HORSE	P05001 equus cabal
11	257	29.4	184	1 INA1_HORSE	P05003 equus cabal
12	257	29.4	184	1 INA3_HORSE	P05005 equus cabal
13	257	29.4	184	1 INA4_HORSE	P05006 equus cabal
14	255.5	29.2	195	1 INT_CEREL	O46633 cervus elap
15	253	28.9	184	1 INA2_HORSE	P05004 equus cabal
16	250.5	28.7	189	1 INAF_HUMAN	P05015 homo sapien
17	247.5	28.3	195	1 INO1_BOVIN	P07352 bos taurus
18	246.5	28.2	172	1 INT2_BOVIN	P56830 bos taurus
19	245.5	28.1	195	1 INT6_SHEEP	Q29429 ovis aries
20	244.5	28.0	188	1 INA2_HUMAN	P01563 homo sapien
21	244	27.9	195	1 INO1_HUMAN	P05000 homo sapien
22	243.5	27.9	189	1 INA4_HUMAN	P05014 homo sapien
23	243.5	27.9	195	1 INT1_SHEEP	P56828 ovis aries
24	243.5	27.9	195	1 INT2_SHEEP	P56829 ovis aries
25	241.5	27.6	189	1 INA5_HUMAN	P01569 homo sapien
26	241.5	27.6	189	1 INA7_HUMAN	P01567 homo sapien
27	240.5	27.5	195	1 INT5_SHEEP	Q28595 ovis aries
28	239.5	27.4	172	1 INT3_BOVIN	P56831 bos taurus
29	239.5	27.4	195	1 INT1_BOVIN	P15696 bos taurus
30	239.5	27.4	195	1 INT7_SHEEP	Q08071 ovis aries
31	239.5	27.4	195	1 INTB_SHEEP	P28169 ovis aries
32	238.5	27.3	189	1 INAG_HUMAN	P01571 homo sapien
33	238.5	27.3	195	1 INT4_SHEEP	Q28594 ovis aries

ALIGNMENTS

RESULT 1

INB\_HUMAN

ID	INB_HUMAN	STANDARD;	PRT;	187 AA.
AC	P01574;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Interferon beta precursor (IFN-beta) (Fibroblast interferon).			
GN	IFNB1 OR IFNB OR IFB.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81198952; PubMed=6164984;			
RA	Lawn R.M., Adelman J., Franke A.E., Houck C.M., Gross M.,			
RA	Najarian R., Goeddel D.V.;			
RT	"Human fibroblast interferon gene lacks introns.";			
RL	Nucleic Acids Res. 9:1045-1052(1981).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Ohno S., Taniguchi T.;			
RT	"Structure of a chromosomal gene for human interferon beta.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 78:5305-5309(1981).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81005095; PubMed=6157601;			
RA	Taniguchi T., Ohno S., Fujii-Kuriyama Y., Muramatsu M.;			
RT	"The nucleotide sequence of human fibroblast interferon cDNA.";			
RL	Gene 10:11-15(1980).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=80254542; PubMed=6157094;			
RA	Derynck R., Content J., Declercq E., Volckaert G., Tavernier J.,			
RA	Devos R., Fiers W.;			
RT	"Isolation and structure of a human fibroblast interferon gene.";			
RL	Nature 285:542-547(1980).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81053720; PubMed=6159580;			
RA	Houghton M., Eaton M.A.W., Stewart A.G., Smith J.C., Doel S.M.,			
RA	Cartlin G.H., Lewis H.M., Patel T.P., Emtage J.S., Carey N.H.,			
RA	Porter A.G.;			
RT	"The complete amino acid sequence of human fibroblast interferon as			
RT	deduced using synthetic oligodeoxynucleotide primers of reverse			
RT	transcriptase.";			
RL	Nucleic Acids Res. 8:2885-2894(1980).			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81053752; PubMed=6159584;			
RA	Goeddel D.V., Shepard H.M., Yelverton E., Leung D., Crea R., Sloma A.,			
RA	Pestka S.;			
RT	"Synthesis of human fibroblast interferon by E. coli.";			
RL	Nucleic Acids Res. 8:4057-4074(1980).			
RN	[7]			

P01570	homo sapien
P37290	homo sapien
Q95187	giraffa cam
P56832	ovis aries
Q08070	ovis aries
P01566	homo sapien
P28171	capra hircu
P28172	ovibos mosc
P05013	homo sapien
Q08072	ovis aries
Q08053	ovis aries
P01568	homo sapien

RP SEQUENCE FROM N.A.  
RX MEDLINE-86035565; PubMed-2414376;  
RA May L.T., Sehgal P.B.;  
RT "On the relationship between human interferon alpha 1 and beta 1  
RT genes";  
RL J. Interferon Res. 5:521-526(1985).  
RN [8]  
RP SEQUENCE OF 1-68 FROM N.A.  
RX MEDLINE-81053854; PubMed-6159597;  
RA Houghton M., Stewart A.G., Doel S.M., Emtage J.S., Eaton M.A.W.,  
RA Smith J.C., Patel T.P., Lewis H.M., Porter A.G., Birch J.R.,  
RA Cartwright T., Carey N.H.;  
RT "The amino-terminal sequence of human fibroblast interferon as  
RT deduced from reverse transcripts obtained using synthetic  
RT oligonucleotide primers";  
RL Nucleic Acids Res. 8:1913-1931(1980).  
RN [9]  
RP DISULFIDE BOND.  
RX MEDLINE-81123083; PubMed-6162107;  
RA Wetzel R.;  
RT "Assignment of the disulphide bonds of leukocyte interferon.";  
RL Nature 289:606-607(1981).  
RN [10]  
RP SEQUENCE OF 71-187 FROM N.A. (VARIANT CLONE PF526).  
RX MEDLINE-82080683; PubMed-6171735;  
RA Shepard H.M., Leung D., Stebbing N., Goeddel D.V.;  
RT "A single amino acid change in IFN-beta1 abolishes its antiviral  
RT activity";  
RL Nature 294:563-565(1981).  
RN [11]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RX MEDLINE-98004481; PubMed-9342320;  
RA Karpusas M., Nolte M., Benton C.B., Meier W., Lipscomb W.N., Goelz S.;  
RT "The crystal structure of human interferon beta at 2.2-A resolution";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:11813-11818(1997).  
CC -!- FUNCTION: HAS ANTIVIRAL, ANTIBACTERIAL AND ANTICANCER ACTIVITIES.  
CC -!- SUBUNIT: MONOMER.  
CC -!- PHARMACEUTICAL: Available under the names Avonex (Biogen),  
CC Betaseron (Berlex) and Rebif (Serono). Used in the treatment of  
CC multiple sclerosis (MS). Betaseron is a slightly modified form  
CC of IFNB1 with two residue substitutions.  
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
CC FAMILY.  
CC -!- DATABASE: NAME=Avonex; NOTE=Clinical information on Avonex;  
CC WWW="http://www.avonex.com/".  
CC -!- DATABASE: NAME=Betaseron; NOTE=Clinical information on Betaseron;  
CC WWW="http://www.betaseron.com/PI.html".  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; V00534; CAA23795.1; -.  
DR EMBL; V00535; CAA23796.1; -.  
DR EMBL; V00546; CAA23807.1; -.  
DR EMBL; V00547; CAA23808.1; -.  
DR EMBL; M28622; AAA36040.1; -.  
DR PIR; A01838; IVHUB1.  
DR PDB; 1AUI; 17-JUN-98.  
DR MIM; 147640; -.  
DR InterPro; IPR000471; Interferon\_abd.  
DR Pfam; PF00143; interferon; 1.  
DR PRINTS; PR00266; INTERFERONAB.  
DR ProDom; PD000550; Interferon\_abd; 1.  
DR SMART; SM00076; IFabd; 1.  
DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
KW Cytokine; Glycoprotein; Antiviral; Signal; Pharmaceutical;  
KW 3d-structure.  
FT SIGNAL 1 21

FT CHAIN 22 187 INTERFERON BETA.  
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .).  
FT DISULFID 52 162  
FT VARIANT 162 162 C -> Y (IN CLONE PF526, LOSS OF ABILITY  
FT TO FORM THE ESSENTIAL DISULFIDE BOND,  
FT LOSS OF ANTIVIRAL ACTIVITY).  
FT /FTid=VAR\_004016.  
SQ SEQUENCE 187 AA; 22294 MW; 0B013D4087723CEC CRC64;  
  
Query Match 98.9%; Score 864; DB 1; Length 187;  
Best Local Similarity 98.8%; Pred. No. 6.8e-65;  
Matches 164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 MSYNLLGFLQSSNFQCQLLWQLNGRLEYCLKDRMNFDPPEIKQLQnFsKEDAALTYI 60  
Db 22 MSYNLLGFLQSSNFQCQLLWQLNGRLEYCLKDRMNFDPPEIKQLQFQKEDAALTYI 81  
  
QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120  
Db 82 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 141  
  
QY 121 HLKRYYGRIHLHYLKAKEYSHCAWTIVRVEILNRFYFNRLTGYLRN 166  
Db 142 HLKRYYGRIHLHYLKAKEYSHCAWTIVRVEILNRFYFNRLTGYLRN 187  
  
RESULT 2  
INB\_FELCA STANDARD; PRT; 186 AA.  
AC Q9N2J0;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Interferon beta precursor (IFN-beta).  
GN IFNB.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Murakami Y., Kubota T., Mochizuki M., Kishi M.;  
RT "Genetic structure of feline interferon beta.";  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: HAS ANTIVIRAL, ANTIBACTERIAL AND ANTICANCER ACTIVITIES  
CC (BY SIMILARITY).  
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
CC FAMILY.  
CC -----  
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CC -----  
DR EMBL; AB021707; BAA93629.1; -.  
DR InterPro; IPR000471; Interferon\_abd.  
DR Pfam; PF00143; interferon; 1.  
DR PRINTS; PR00266; INTERFERONAB.  
DR ProDom; PD000550; Interferon\_abd; 1.  
DR SMART; SM00076; IFabd; 1.  
DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
KW Cytokine; Antiviral; Glycoprotein; Signal.  
FT SIGNAL 1 21  
FT CHAIN 22 186 INTERFERON BETA.  
FT DISULFID 52 161 BY SIMILARITY.  
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).



```
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 186 AA; 22187 MW; 25C359B1808AC862 CRC64;

Query Match
Best Local Similarity 59.1%; Score 516.5; DB 1; Length 186;
Matches 101; Conservative 26; Mismatches 38; Indels 1; Gaps 1;

QY 1 MSYNLLGFLQRSSNFQCKLLWQLNGRLEYCLKDRMNFDPPEEIKQLQnFskEDAALTIY 60
Db 22 VSYKLLGFLQRSSSLECELLVNLNRTSKYCLKDRMNFPEVPEEIKKSQRQKEAILVIN 81

QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
Db 82 EMFQKIFNIFSRSTSTGWNETIVENLLATLHWQKEHLEETILEEIMEEENFTWDN-TTLL 140

QY 121 HLKRYYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLRN 166
Db 141 NLKKYYLRIVRYLKAKEYSVCAWTVVHAEILRNFFFLERLTDYLRN 186

RESULT 3
INB2_BOVIN
ID INB2_BOVIN STANDARD; PRT; 186 AA.
AC P01576;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Interferon beta-2 precursor.
GN IFNB2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Leung D.W., Capon D.J., Goeddel D.V.;
RT "The structure and bacterial expression of three distinct bovine
interferon-beta genes.";
RL Biotechnology 2:458-464(1984).
CC -!- FUNCTION: HAS ANTIVIRAL, ANTIBACTERIAL AND ANTICANCER ACTIVITIES.
CC -!- SUBUNIT: MONOMER.
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
FAMILY.
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DR EMBL; M15478; AAA30580.1; -.
DR PIR; A01840; IVB0B2.
DR HSSP; P01574; 1AU1.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Cytokine; Glycoprotein; Antiviral; Multigene family; Signal.
FT SIGNAL 1 21
FT CHAIN 22 186 INTERFERON BETA-2.
FT DISULFID 52 161 PROBABLE.
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 186 AA; 22319 MW; D9F257C63250480 CRC64;

Query Match
Best Local Similarity 55.2%; Score 482.5; DB 1; Length 186;
Matches 96; Conservative 27; Mismatches 42; Indels 1; Gaps 1;
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Best Local Similarity 56.7%; Pred. No. 2.4e-33;
Matches 93; Conservative 30; Mismatches 40; Indels 1; Gaps 1;

QY 2 SYNLLGFLQRSSNFQCKLLWQLNGRLEYCLKDRMNFDPPEEIKQLQnFskEDAALTIYE 61
Db 23 SYSLRFQQRSLALCQKLLRQLPSTPQHCLREARMDQMPEEMKQAQFQKEDAILVIYE 82

QY 62 MLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLH 121
Db 83 MLQQIFNILTRDFSSTGWSSETIIEDLEELYEQMNHLEPIQKEIMQKQNSTMGD-TTVLH 141

QY 122 LKRYGRIHLHYLKAKEYSHCAWTIVRVEILRNFFYNRLTGYLR 165
Db 142 LRKYFNLVQYLLKSKEYNRCAWTVVVRVQVILRNFSFLTRLTGYLR 185

RESULT 4
INB_HORSE
ID INB_HORSE STANDARD; PRT; 186 AA.
AC P05012;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Interferon beta precursor (IFN-beta).
GN IFNB.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87053170; Pubmed=3022999;
RA Himmler A., Hauptmann R., Adolf G.R., Swetly P.;
RT "Molecular cloning and expression in Escherichia coli of equine type
I interferons.";
RL DNA 5:345-356(1986).
CC -!- FUNCTION: HAS ANTIVIRAL, ANTIBACTERIAL AND ANTICANCER ACTIVITIES.
CC -!- SUBUNIT: MONOMER.
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
FAMILY.
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DR EMBL; M14546; AAA30954.1; -.
DR PIR; G24912; IVH0BI.
DR HSSP; P01574; 1AU1.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Cytokine; Antiviral; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 186 INTERFERON BETA.
FT DISULFID 52 161 BY SIMILARITY.
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 186 AA; 21882 MW; AE9F3ADF006EE6C CRC64;

Query Match
Best Local Similarity 54.6%; Score 477.5; DB 1; Length 186;
Matches 96; Conservative 27; Mismatches 42; Indels 1; Gaps 1;

QY 1 MSYNLLGFLQRSSNFQCKLLWQLNGRLEYCLKDRMNFDPPEEIKQLQnFskEDAALTIY 60
Db 22 VSYKLLGFLQRSSSLECELLVNLNRTSKYCLKDRMNFPEVPEEIKKSQRQKEAILVIN 81
```

Db 22 VNYDLRSQRSSNSACLMLLRQLNGAPQRCPEDTMNFQVPEIEQAQQFKEDAAALVIY 81

QY 61 EMLQNIFAIFRQDSSSTGWNETHIVNLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120

Db 82 EMLQHTWIRFRNFASFGWNETIVKNLLVEVHLQMDRLETNLEETMEESSTWGN-TTIL 140

QY 121 HLKRYGGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLNRN 166

Db 141 RLKYYGRISQYLKAKKYSCHCAWTVVQAEMLRNLAFLNGLTDYLQN 186

RESULT 5

INB3\_BOVIN

ID INB3\_BOVIN STANDARD; PRT; 186 AA.

AC P01577;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Interferon beta-3 precursor.

GN IFNB3.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RA Leung D.W., Capon D.J., Goeddel D.V.;

RT "The structure and bacterial expression of three distinct bovine interferon-beta genes.";

RL Biotechnology 2:458-464(1984).

CC -|- FUNCTION: HAS ANTIVIRAL, ANTIBACTERIAL AND ANTICANCER ACTIVITIES.

CC -|- SUBUNIT: MONOMER.

CC -|- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA FAMILY.

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CC -----

DR EMBL; M15479; AAA30581.1; -.

DR PIR; A01841; IVBOB3.

DR HSSP; P01574; 1AU1.

DR InterPro; IPR000471; Interferon\_abd.

DR Pfam; PF00143; Interferon; 1.

DR PRINTS; PR00266; INTERFERONAB.

DR ProDom; PD000550; Interferon\_abd; 1.

DR SMART; SM00076; IFabd; 1.

DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.

KW Cytokine; Glycoprotein; Antiviral; Multigene family; Signal.

FT SIGNAL 1 21

FT CHAIN 22 186 INTERFERON BETA-3.

FT DISULFID 52 161 PROBABLE.

FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 186 AA; 22059 MW; 1D10111EBE1A65D CRC64;

Query Match 51.7%; Score 451.5; DB 1; Length 186;

Best Local Similarity 52.7%; Pred. No. 9e-31;

Matches 87; Conservative 34; Mismatches 43; Indels 1; Gaps 1;

QY 2 SYNLLGFLQRSSNFQCKLLWQLNGRLEYCLKDRMNFDPPEIKQLQnFskEDAALTIYE 61

Db 23 SYSLLRFQRRSAEVCQKLLGLHSTPQHCLAKMDFQVPEEMNAQQFRKEDAILVIYE 82

QY 62 MLQNIFAIFRQDSSSTGWNETHIVNLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLH 121

Db 83 MLQQIFNLTDRDSSSTGWSERTIEDLLVELYGMNRLQPIQKEIMQEQNFTMGD-TTVLH 141

QY 122 LKRYGGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLNRN 166

Db 142 LKYYFNLVQYLESKEYNRCATVVRVQILTNFSLMRLTASLRD 186

RESULT 6

INB1\_BOVIN

ID INB1\_BOVIN STANDARD; PRT; 186 AA.

AC P01578;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Interferon beta-1 precursor.

GN IFNB1.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RA Leung D.W., Capon D.J., Goeddel D.V.;

RT "The structure and bacterial expression of three distinct bovine interferon-beta genes.";

RL Biotechnology 2:458-464(1984).

CC -|- FUNCTION: HAS ANTIVIRAL, ANTIBACTERIAL AND ANTICANCER ACTIVITIES.

CC -|- SUBUNIT: MONOMER.

CC -|- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA FAMILY.

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CC -----

DR EMBL; M15477; AAA30579.1; -.

DR PIR; A01842; IVBOB1.

DR HSSP; P01574; 1AU1.

DR InterPro; IPR000471; Interferon\_abd.

DR Pfam; PF00143; Interferon; 1.

DR PRINTS; PR00266; INTERFERONAB.

DR ProDom; PD000550; Interferon\_abd; 1.

DR SMART; SM00076; IFabd; 1.

DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.

KW Cytokine; Glycoprotein; Antiviral; Multigene family; Signal.

FT SIGNAL 1 21

FT CHAIN 22 186 INTERFERON BETA-1.

FT DISULFID 52 161 PROBABLE.

FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 186 AA; 22195 MW; F9060C07EA415B9C CRC64;

Query Match 49.3%; Score 430.5; DB 1; Length 186;

Best Local Similarity 50.3%; Pred. No. 4.9e-29;

Matches 83; Conservative 36; Mismatches 45; Indels 1; Gaps 1;

QY 2 SYNLLGFLQRSSNFQCKLLWQLNGRLEYCLKDRMNFDPPEIKQLQnFskEDAALTIYE 61

Db 23 SYSLLRFQRRSQSLKECQKLLGLPLSTPSQHCLFARMDFQPMPEMKQEQFQKEDAILVMYE 82

QY 62 MLQNIFAIFRQDSSSTGWNETHIVNLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLH 121

Db 83 VLQHFILTRDSSSTGWSERTIEDLLKELYQMNRLOPIQKEIMQKQNSTEDTIVP-H 141

QY 122 LKRYGGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLNRN 166

Db 142 LGKYYFNLMQYLESKEYDRCAWTVVQVQILTNVSELMRLTGYVRD 186

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RESULT 7
INB_MOUSE
ID INB_MOUSE STANDARD; PRT; 182 AA.
AC P01575;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interferon beta precursor (IFN-beta).
GN IFNB OR IFB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83265757; PubMed=6688252;
RA Higashi Y., Sokawa Y., Watanabe Y., Kawade Y., Ohno S., Takaoka C.,
RA Taniguchi T.;
RT "Structure and expression of a cloned cDNA for mouse interferon-
RT beta.";
RL J. Biol. Chem. 258:9522-9529(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89263735; PubMed=2726460;
RA Kuga T., Fujita T., Taniguchi T.;
RT "Nucleotide sequence of the mouse interferon-beta gene.";
RL Nucleic Acids Res. 17:3291-3291(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89125582; PubMed=3221389;
RA Vojdani G., Coulombel C., Doly J.;
RT "Structure and characterization of a murine chromosomal fragment
RT containing the interferon beta gene.";
RL J. Mol. Biol. 204:221-231(1988).
RN [4]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=88196115; PubMed=3360010;
RA Civas A., Fournet B., Coulombel C., le Roscouet D., Honvault A.,
RA Petek F., Montreuil J., Doly J.;
RT "Purification and carbohydrate structure of natural murine
RT interferon-beta.";
RL Eur. J. Biochem. 173:311-316(1988).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.75 ANGSTROMS).
RA Senda T., Matsuda S., Kurihara H., Nakamura K.T., Kawano G.,
RA Shimizu H., Mizuno H., Mitsui Y.;
RT "Three-dimensional structure of recombinant murine interferon-beta.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 66:77-80(1990).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=92371425; PubMed=1505514;
RA Senda T., Shimazu T., Matsuda S., Kawano G., Shimizu H.,
RA Nakamura K.T., Mitsui Y.;
RT "Three-dimensional crystal structure of recombinant murine interferon-
RT beta.";
RL EMBO J. 11:3193-3201(1992).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS).
RX MEDLINE=96028219; PubMed=7473712;
RA Senda T., Saitoh S.-I., Mitsui Y.;
RT "Refined crystal structure of recombinant murine interferon-beta at
RT 2.15-A resolution.";
RL J. Mol. Biol. 253:187-207(1995).
CC -1- FUNCTION: HAS ANTIVIRAL, ANTIBACTERIAL AND ANTICANCER ACTIVITIES.
CC -1- SUBUNIT: MONOMER.
CC -1- PTM: THIS BETA INTERFERON DOES NOT HAVE A DISULFIDE BOND.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
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DR EMBL; K00020; AAA37891.1; -
DR EMBL; X14455; CAA32625.1; -
DR EMBL; X14029; CAA32190.1; -
DR PIR; A01839; IVMSB.
DR PIR; S02020; S02020.
DR PDB; 1IFA; 31-JAN-94.
DR PDB; 2HIF; 31-AUG-94.
DR PDB; 1RMI; 14-FEB-95.
DR MGD; MGI:107657; Ifnb.
DR InterPro; IPR000471; Interferon_abd.
DR Pfam; PF00143; interferon; 1.
DR PRINTS; PR00266; INTERFERONAB.
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Cytokine; Glycoprotein; Antiviral; Signal; 3D-structure.
FT SIGNAL 1 21
FT CHAIN 22 182 INTERFERON BETA.
FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 182 AA; 22127 MW; 8C4C32947FD1B917 CRC64;

Query Match 38.5%; Score 336.5; DB 1; Length 182;
Best Local Similarity 45.8%; Pred. No. 2.9e-21;
Matches 76; Conservative 26; Mismatches 59; Indels 5; Gaps 3;

QY 1 MSYNLLGFLQSSNFQCKLLWQLNGRLLEYCLKDRMFDIPEEIKQLQnFsKEDAAALTIY 60
   :| | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 22 INYKQLQEQERTNIRKCCQELLEQLNGKIN--LTYRADFKIPMEM--TEKMQKSYTAFAIQ 77

QY 61 EMLQNIFFAIFRDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120
   ||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 78 EMLQNVFLVFRNFSSTGWNETIVVRLLDLHQQTVFLKTVLEEK-QEERLTWEMSSAL 136

QY 121 HLKRYVGRILHYLKAKEYSHCAWTVRVEILRNFFYNRLTGILRN 166
   ||| ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 137 HLKSYVRVQRYLKLKYNKYSAWVVAEIRFNLIRRLTRNFQN 182

RESULT 8
INB_RAT
ID INB_RAT STANDARD; PRT; 184 AA.
AC P70499;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Interferon beta precursor (IFN-beta).
GN IFNB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=Liver;
RX MEDLINE=97271387; PubMed=9126338;
RA Yokoyama S., Ohishi N., Shamoto M., Watanabe Y., Yagi K.;
RT "Isolation and expression of rat interferon beta gene and growth-
RT inhibitory effect of its expression on rat glioma cells.";
RL Biochem. Biophys. Res. Commun. 232:698-701(1997).
CC -1- FUNCTION: HAS ANTIVIRAL, ANTIBACTERIAL AND ANTICANCER ACTIVITIES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- PTM: THIS BETA INTERFERON DOES NOT HAVE A DISULFIDE BOND.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
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CC -----

DR EMBL; D87919; BAA13502.1; -.  
DR HSSP; P01575; 2HIF.  
DR InterPro; IPR000471; Interferon\_abd.  
DR Pfam; PF00143; Interferon; 1.  
DR PRINTS; PR00266; INTERFERONAB.  
DR ProDom; PD000550; Interferon\_abd; 1.  
DR SMART; SM00076; IFabd; 1.  
DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
KW Cytokine; Antiviral; Glycoprotein; Signal.  
FT SIGNAL 1 21 BY SIMILARITY.  
FT CHAIN 22 184 INTERFERON BETA.  
FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 184 AA; 22072 MW; 1D051D29F979ADDE CRC64;

Query Match 37.6%; Score 328.5; DB 1; Length 184;  
Best Local Similarity 45.2%; Pred. No. 1.3e-20;  
Matches 75; Conservative 23; Mismatches 65; Indels 3; Gaps 2;

QY 1 MSYNLLGFLQRSSNFQCQLLWQLNGRLEYCLKDRMNFDPPEIKQLQnFsKEDAALTIY 60  
Db 22 IDYKQLQFRQSTIRTCQKLLRQLNGRLN--LSYRTDFKIPMEVMPHPSQMEKSYTAFAIQ 79  
QY 61 EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSL 120  
Db 80 VMLQNVFLVFRSFSSTGWNETIVESLLDELHQQTLELLEILKEK-QEERLTWVTSTTIL 138  
QY 121 HLKRYYGRIHLHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGVLN 166  
Db 139 GLKSYWRVQRYLKDKKYNSYAMVVRVRAEVRNFESIILRLNRFQN 184

RESULT 9  
INO2\_HORSE  
ID INO2\_HORSE STANDARD; PRT; 195 AA.  
AC P05002;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 01-APR-1988 (Rel. 07, Last annotation update)  
DE Interferon omega-2 precursor (Interferon alpha-II-2).  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE OF 167-195 FROM N.A.  
RX MEDLINE=87053170; PubMed=3022999;  
RA Himmeler A., Hauptmann R., Adolf G.R., Swetly P.;  
RT "Molecular cloning and expression in Escherichia coli of equine type  
RT I interferons.";  
RL DNA 5:345-356(1986).  
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
CC FAMILY.  
CC -----

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CC -----

DR EMBL; M14545; AAA30949.1; -.  
DR EMBL; A16557; CAA01293.1; -.  
DR PIR; F24912; IVHO22.  
DR HSSP; P01563; 2HIE.  
DR InterPro; IPR000471; Interferon\_abd.  
DR Pfam; PF00143; Interferon; 1.  
DR PRINTS; PR00266; INTERFERONAB.  
DR ProDom; PD000550; Interferon\_abd; 1.  
DR SMART; SM00076; IFabd; 1.  
DR PROSITE; PS00252; INTERFERON\_A\_B\_D; 1.  
KW Cytokine; Glycoprotein; Antiviral; Multigene family; Signal.  
FT SIGNAL 1 23  
FT CHAIN 24 195 INTERFERON OMEGA-2.  
FT DISULFID 24 122 BY SIMILARITY.  
FT DISULFID 52 162 BY SIMILARITY.  
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 195 AA; 22131 MW; 949DA221AB3C17DF CRC64;

Query Match 32.5%; Score 284; DB 1; Length 195;  
Best Local Similarity 36.6%; Pred. No. 6.8e-17;  
Matches 60; Conservative 33; Mismatches 57; Indels 14; Gaps 1;

QY 2 SYNLLGFLQRSSNFQCQLLWQLNGRLEYCLKDRMNFDPPEIKQLQnFsKEDAALTIYE 61  
Db 37 NFVLLGQMSRISS-----AICLKDKDFRPQDMADGRQFPEAQAAASVLHE 82  
QY 62 MLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLH 121  
Db 83 MLQIIFSLFHTERSAAWNTLLDELCTGLLRQLEDLDTCLCEQEMGEESALGTVRPTLA 142  
QY 122 LKRYYGRIHLHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRL 165  
Db 143 VKRYFRGIHLHYLKEKKYSDCAWEIVRMEIRMSFSSSANLQGRRLR 186

RESULT 10  
INO1\_HORSE  
ID INO1\_HORSE STANDARD; PRT; 195 AA.  
AC P05001;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 01-APR-1988 (Rel. 07, Last annotation update)  
DE Interferon omega-1 precursor (Interferon alpha-II-1).  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87053170; PubMed=3022999;  
RA Himmeler A., Hauptmann R., Adolf G.R., Swetly P.;  
RT "Molecular cloning and expression in Escherichia coli of equine type  
RT I interferons.";  
RL DNA 5:345-356(1986).  
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA  
CC FAMILY.  
CC -----

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CC -----

DR EMBL; M14544; AAA30955.1; -.  
DR EMBL; A15991; CAA01259.1; -.  
DR PIR; E24912; IVHO21.  
DR HSSP; P01563; 2HIE.  
DR InterPro; IPR000471; Interferon\_abd.  
DR Pfam; PF00143; Interferon; 1.  
DR PRINTS; PR00266; INTERFERONAB.



```
DR ProDom; PD000550; Interferon_abd; 1.
DR SMART; SM00076; IFabd; 1.
DR PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Cytokine; Glycoprotein; Antiviral; Multigene family; Signal.
FT SIGNAL 1 23
FT CHAIN 24 195 INTERFERON OMEGA-1.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
FT CARBOHYD 101 101 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 195 AA; 21882 MW; A81C3CF0A7CA9B6E CRC64;

Query Match 30.1%; Score 263; DB 1; Length 195;
Best Local Similarity 40.3%; Pred. No. 3.7e-15;
Matches 54; Conservative 26; Mismatches 54; Indels 0; Gaps 0;

QY 31 CLKDRMNFDIPEEIKQLQnFsKEDAAALTIYEMLQNIFAIFRQDSSSTGWNETIVENLLAN 90
Db 52 CLKHRTDFRFPQEQLDGRQFPEAQATSVLQEMLQIVSLFHTERSAAWNTLLDRLLAG 111
QY 91 VYHQINHLKTVLEEKLEKEDFTRGKLMSSLHLKRYVGRILHYLKAKEYSHCAWTIVRVEI 150
Db 112 LHQOLEDLNTCLDEQTGEESALGTGVTPLAVKRYFRIRLYLTEKKYSDCAWEIVRVDI 171
QY 151 LRNFYFINRLTGYL 164
Db 172 MRSFSSSANLQGR 185

RESULT 11
INAL_HORSE
ID INAL_HORSE STANDARD; PRT; 184 AA.
AC P05003;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Interferon alpha-1 precursor.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87053170; PubMed=3022999;
RA Himmler A., Hauptmann R., Adolf G.R., Swetly P.;
RT "Molecular cloning and expression in Escherichia coli of equine type I interferons.";
RL DNA 5:345-356(1986).
CC -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
CC
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CC
CC EMBL; M14540; AAA30953.1; -.
CC PIR; A24912; IVHOA1.
CC HSSP; P01563; 2HIE.
CC InterPro; IPR000471; Interferon_abd.
CC Pfam; PF00143; Interferon; 1.
CC PRINTS; PR00266; INTERFERONAB.
CC ProDom; PD000550; Interferon_abd; 1.
CC SMART; SM00076; IFabd; 1.
CC PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Cytokine; Antiviral; Multigene family; Signal.
FT SIGNAL 1 23
```

```
FT CHAIN 24 184 INTERFERON ALPHA-1.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
SQ SEQUENCE 184 AA; 20808 MW; 9E860B8CD05C83E6 CRC64;

Query Match 29.4%; Score 257; DB 1; Length 184;
Best Local Similarity 36.0%; Pred. No. 1.1e-14;
Matches 54; Conservative 28; Mismatches 54; Indels 14; Gaps 1;

QY 5 LLGFLQRSSNFQCKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQnFsKEDAAALTIYEMLQ 64
Db 40 LLGQMRRI SPFS-----CLKDRNDFGFPQEVFDGNQFRKPKQALSAVHETIQ 85
QY 65 NIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLHLKR 124
Db 86 QIFHLFSTDGSSAAWDESLDKLYTGLYQQLTELEACLSQEVGVEETPLMNEDSLLAVRR 145
QY 125 YVGRILHYLKAKEYSHCAWTIVRVEILRNF 154
Db 146 YFORIALYLQEKKYSPCAWEIVRAEIMRSF 175

RESULT 12
INA3_HORSE
ID INA3_HORSE STANDARD; PRT; 184 AA.
AC P05005;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Interferon alpha-3 precursor.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87053170; PubMed=3022999;
RA Himmler A., Hauptmann R., Adolf G.R., Swetly P.;
RT "Molecular cloning and expression in Escherichia coli of equine type I interferons.";
RL DNA 5:345-356(1986).
CC -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
CC
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CC
CC EMBL; M14542; AAA30951.1; -.
CC PIR; C24912; IVHOA3.
CC HSSP; P01563; 2HIE.
CC InterPro; IPR000471; Interferon_abd.
CC Pfam; PF00143; Interferon; 1.
CC PRINTS; PR00266; INTERFERONAB.
CC ProDom; PD000550; Interferon_abd; 1.
CC SMART; SM00076; IFabd; 1.
CC PROSITE; PS00252; INTERFERON_A_B_D; 1.
KW Cytokine; Antiviral; Multigene family; Signal.
FT SIGNAL 1 23
FT CHAIN 24 184 INTERFERON ALPHA-3.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
SQ SEQUENCE 184 AA; 20782 MW; 4C15D991ECA6D24A CRC64;
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Query Match 29.4%; Score 257; DB 1; Length 184;  
Best Local Similarity 36.0%; Pred. No. 1.1e-14;  
Matches 54; Conservative 28; Mismatches 54; Indels 14; Gaps 1;

QY	5	LLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDP	EEIKQLQNFsKEDAAALTIYEMLQ	64
		:		
Db	40	LLGQMRRI	SPFS-----CLKDRNDFGFPQEVFDGNQFRK	QPAISAVHETIQ 85
QY	65	NIFAIFRQDSSSTGWN	TIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLHLKR	124
		:		
Db	86	QIFHLFSTDGSSAAW	DESLLDKLYTGLYQQLTEACL	SQEVGVETPLMNEDSLLAVRR 145
QY	125	YYGRILHYLKAKEYSHCAWTIVRVEILRNF	154	
		:		
Db	146	YFQRIALYLQEKKYSPCAWEIVRAEIMRSF	175	

RESULT 13				
INA4_HORSE				
ID	INA4_HORSE	STANDARD;	PRT;	184 AA.
AC	P05006;			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	01-MAR-1989 (Rel. 10, Last annotation update)			
DE	Interferon alpha-4 precursor.			
OS	Equus caballus (Horse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.			
OX	NCBI_TaxID=9796;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87053170; Pubmed=3022999;			
RA	Himmler A., Hauptmann R., Adolf G.R., Swetly P.;			
RT	"Molecular cloning and expression in Escherichia coli of equine type I interferons.";			
RL	DNA 5:345-356(1986).			
CC	-1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES: A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.			
CC	-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA FAMILY.			

CC	-----			
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CC	-----			
DR	EMBL; M14543; AAA30952.1; -.			
DR	PIR; D24912; IVHOA4.			
DR	HSSP; P01563; 2HIE.			
DR	InterPro; IPR000471; Interferon_abd.			
DR	Pfam; PF00143; Interferon; 1.			
DR	PRINTS; PR00266; INTERFERONAB.			
DR	ProDom; PD000550; Interferon_abd; 1.			
DR	SMART; SM00076; IFabd; 1.			
DR	PROSITE; PS00252; INTERFERON_A_B_D; 1.			
KW	Cytokine; Antiviral; Multigene family; Signal.			
FT	SIGNAL 1 23			
FT	CHAIN 24 184 INTERFERON ALPHA-4.			
FT	DISULFID 24 122 BY SIMILARITY.			
FT	DISULFID 52 162 BY SIMILARITY.			
SQ	SEQUENCE 184 AA; 20860 MW; FC087F46F11C68EC CRC64;			

Query Match 29.4%; Score 257; DB 1; Length 184;  
Best Local Similarity 36.0%; Pred. No. 1.1e-14;  
Matches 54; Conservative 28; Mismatches 54; Indels 14; Gaps 1;

QY	5	LLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDP	EEIKQLQNFsKEDAAALTIYEMLQ	64
----	---	--------------------------------------	--------------------------	----

Db	40	LLGQMRRI	SPFS-----CLKDRNDFGFPQEVFDGNQFRK	QPAISAVHETIQ 85
QY	65	NIFAIFRQDSSSTGWN	TIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLHLKR	124
		:		
Db	86	QIFHLFSTDGSSAAW	DESLLDKLYTGLYQQLTEACL	SQEVGVETPLMNEDSLLAVRR 145
QY	125	YYGRILHYLKAKEYSHCAWTIVRVEILRNF	154	
		:		
Db	146	YFQRIALYLQEKKYSPCAWEIVRAEIMRSF	175	

RESULT 14				
INT_CEREL				
ID	INT_CEREL	STANDARD;	PRT;	195 AA.
AC	O46633;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Interferon tau precursor (IFN-tau) (Trophoblast protein-1) (TP-1) (Trophoblastin) (Antiluteolysin) (Trophoblast antiluteolytic protein).			
GN	IFNT.			
OS	Cervus elaphus (Red deer).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;			
OC	Cervidae; Cervinae; Cervus.			
OX	NCBI_TaxID=9860;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99273269; PubMed=10341723;			
RA	Demmers K.J., Kaluz S., Deakin D.W., Jabbour H.N., Flint A.P.F.;			
RT	"Production of interferon by the conceptus in red deer Cervus elaphus.";			
RL	J. Reprod. Fert. 115:59-65(1999).			
RN	[2]			
RP	REVIEW.			
RX	MEDLINE=99081096; PubMed=9865498;			
RA	Martal J.L., Chene N.M., Huynh L.P., L'Haridon R.M., Reynaud P.B., Guillomot M.W., Charlier M.A., Charpigny S.Y.;			
RT	"IFN-tau: a novel subtype I IFN1. Structural characteristics, non-ubiquitous expression, structure-function relationships, a pregnancy hormonal embryonic signal and cross-species therapeutic potentialities.";			
RL	Biochimie 80:755-777(1998).			
CC	-1- FUNCTION: PARACRINE HORMONE PRIMARLY RESPONSIBLE FOR MATERNAL RECOGNITION OF PREGNANCY. INTERACTS WITH ENDOMETRIAL RECEPTORS, PROBABLY TYPE I INTERFERON RECEPTORS, AND BLOCKS ESTROGEN RECEPTOR EXPRESSION, PREVENTING THE ESTROGEN-INDUCED INCREASE IN OXYTOCIN RECEPTOR EXPRESSION IN THE ENDOMETRIUM. THIS RESULTS IN THE SUPPRESSION OF THE PULSATILE ENDOMETRIAL RELEASE OF THE LUTEOLYTIC HORMONE PROSTAGLANDIN F2-ALPHA, HINDERING THE REGRESSION OF THE CORPUS LUTEUM (LUTEOLYSIS) AND THEREFORE A RETURN TO OVARIAN CYCLICITY. THIS, AND A POSSIBLE DIRECT EFFECT OF IFN-TAU ON PROSTAGLANDIN SYNTHESIS, LEADS IN TURN TO CONTINUED OVARIAN PROGESTERONE SECRETION, WICH STIMULATES THE SECRETION BY THE ENDOMETRIUM OF THE NUTRIENTS REQUIRED FOR THE GROWTH OF THE CONCEPTUS. IN SUMMARY, DISPLAYS PARTICULARLY HIGH ANTIVIRAL AND ANTIPROLIFERATIVE POTENCY CONCURRENTLY WITH PARTICULAR WEAK CYTOTOXICITY, HIGH ANTILUTEOLYTIC ACTIVITY AND IMMUNOMODULATORY PROPERTIES. IN CONTRAST WITH OTHER IFNS, IFN-TAU IS NOT VIRALLY INDUCIBLE.			
CC	-1- SUBCELLULAR LOCATION: SECRETED INTO THE UTERINE LUMEN.			
CC	-1- TISSUE SPECIFICITY: CONSTITUTIVELY AND EXCLUSIVELY EXPRESSED IN THE MONONUCLEAR CELLS OF THE EXTRA-EMBRYONIC TROPHECTODERM.			
CC	-1- DEVELOPMENTAL STAGE: MAJOR SECRETORY PRODUCT SYNTHESIZED BY THE CONCEPTUS DURING A VERY SHORT PERIOD IN EARLY PREGNANCY.			
CC	-1- MISCELLANEOUS: IFN-TAU GENES ARE INTRONLESS. THEY EVOLVED FROM IFN-OMEGA GENES IN THE RUMINANTIA SUBORDER AND HAVE CONTINUED TO DUPLICATE INDEPENDENTLY IN DIFFERENT LINEAGES OF THE RUMINANTIA. THEY ENCODE FOR PROTEINS VERY SIMILAR IN SEQUENCE BUT WITH DIFFERENT BIOLOGICAL POTENCY AND PATTERN OF EXPRESSION.			
CC	-1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA FAMILY. IFN-ALPHA1 SUBFAMILY.			

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CC -----
CC EMBL; AJ000638; CAA04193.1; -.
CC HSSP; P01563; 2HIE.
CC InterPro; IPR000471; Interferon_abd.
CC Pfam; PF00143; interferon; 1.
CC PRINTS; PR00266; INTERFERONAB.
CC ProDom; PD000550; Interferon_abd; 1.
CC SMART; SM00076; IFabd; 1.
CC PROSITE; PS00252; INTERFERON_A_B_D; 1.
CC pregnancy; Cytokine; Hormone; Antiviral; Signal.
CC SIGNAL 1 23 BY SIMILARITY.
CC CHAIN 24 195 INTERFERON TAU.
CC DISULFID 24 122 BY SIMILARITY.
CC DISULFID 52 162 BY SIMILARITY.
CC SEQUENCE 195 AA; 22075 MW; F5304ACB1ACF0CC7 CRC64;

Query Match 29.2%; Score 255.5; DB 1; Length 195;
Best Local Similarity 37.6%; Pred. No. 1.5e-14;
Matches 56; Conservative 33; Mismatches 57; Indels 3; Gaps 2;

QY 19 KLLWQLNGRL--EYCLKDRMNFDPPEIKQLQFQSKEDAALTIYEMLQNFQFQDSSS 76
   ||| | : || : || : || : || : || : || : || : || : || : || : ||
Db 39 KLLGQMT-RLSPRFCLQDRKDFGLPQEMVEGGQLQKDAQISVLHEMLQQCFNLFHTERS 97
   ||| | : || : || : || : || : || : || : || : || : || : || : ||

QY 77 TGNWETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSHLKRYGRILHYLKAK 136
   | : || : || : || : || : || : || : || : || : || : || : || : ||
Db 98 AAWDTTLLEQLRFGHQQLDDLDACLQGVMGKEDSLRRMGPTLTVKKYFQGIHVYLQEK 157

QY 137 EYSHCAWTIVRVEILRNIFYINRLTGYLK 165
   ||| ||| ||| ||| : || : || : || : || : || : || : || : || : ||
Db 158 EYSDCAWEIVQVEMMRALSSISRLQKRLR 186

RESULT 15
INA2_HORSE
ID INA2_HORSE STANDARD; PRT; 184 AA.
AC P05004;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Interferon alpha-2 precursor.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87053170; PubMed=3022999;
RA Himmeler A., Hauptmann R., Adolf G.R., Sweetly P.;
RT "Molecular cloning and expression in Escherichia coli of equine type
RT I interferons.";
RL DNA 5:345-356(1986).
CC -!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC -!- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY.
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CC -----
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M14541; AAA30950.1; -.
CC EMBL; A15987; CAA01258.1; -.
CC PIR; B24912; IVHOA2.
CC HSSP; P01563; 2HIE.
CC InterPro; IPR000471; Interferon_abd.
CC Pfam; PF00143; interferon; 1.
CC PRINTS; PR00266; INTERFERONAB.
CC ProDom; PD000550; Interferon_abd; 1.
CC SMART; SM00076; IFabd; 1.
CC PROSITE; PS00252; INTERFERON_A_B_D; 1.
CC Cytokine; Antiviral; Multigene family; Signal.
CC SIGNAL 1 23
CC CHAIN 24 184 INTERFERON ALPHA-2.
CC DISULFID 24 122 BY SIMILARITY.
CC DISULFID 52 162 BY SIMILARITY.
CC SEQUENCE 184 AA; 20877 MW; FC15DC7D811C68EC CRC64;

Query Match 28.9%; Score 253; DB 1; Length 184;
Best Local Similarity 36.0%; Pred. No. 2.3e-14;
Matches 54; Conservative 27; Mismatches 55; Indels 14; Gaps 1;

QY 5 LLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDPPEIKQLQFQSKEDAALTIYEMLQ 64
   ||| : || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 40 LLGQMRRIISPFS-----CLKDRNDFGFPQEVDFGNQFRKPQAISAVHETIQ 85
   ||| : || | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 65 NIFAIFRODSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSHLKLR 124
   || : || | | | | : || : || : || : || : || : || : || : || : || : ||
Db 86 QIFHLFSTDGSSAAWDESLLDKLYTGLYQQLTELEACLSQEVGVVEETPLMNEDSLLAVRR 145
   || : || | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 125 YYGRILHYLKKEYSHCAWTIVRVEILRN 154
   | : || ||| : || : || | | | | | | | | | | | | | | | | | | | | | |
Db 146 YFORIALYLQEKKYSPCAWEIVRAEIMRCF 175

Search completed: July 29, 2002, 15:45:11
Job time: 187 sec
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